

FIGURE 1

CGCCCGCGCGCGGGCTCAACTTGTAGAGCGAGGGGCCAACTTGGCAGAGCGCGCGGCCA
GCCTTGAGAGAGCGCCCTCCAGGGACTATGCGTGCAGGGACACGGGATCTACCCATACC
ATTGACTAACTATGGAAGATTATAACAAAATAGAGAAAATTGGAGAAGGTACCTATGGAG
TTGTGTATAAGGGTAGACACAAAACACTACAGGTCAAGTGGTAGCCATGAAAAAAATCAGAC
TAGAAAGTGAAGAGGAAGGGTTCTAGTACTGCAATTGGGAAATTCTCTATTAAAGG
AACTTCGTCATCCAAATATACTAGTCAGTCTCAGGATGTGCTTATGCAGGATTCCAGGTTAT
ATCTCATCTTGAGTTCTTCCATGGATCTGAAGAAAATCTTGGATTCTATCCCTCCTG
GTCAGTACATGGATTCTCACTTGTAAAGGTAGTAACACTCTGGTACAGATCTCCAGAAG
TATTGCTGGGGTCAGCTCGTTACTCAACTCCAGTTGACATTGGAGTATAGGCACCATAT
TTGCTGAACTAGCAACTAAGAAACCACCTTCCATGGGGATTCAAGAAATTGATCAACTCT
TCAGGATTTCAGAGCTTGGGCACTCCCAATAATGAAGTGTGGCCAGAAGTGGAAATCTT
TACAGGACTATAAGAATACATTCCCAATGGAAACCAGGAAGCCTAGCATCCCATGTCA
AAAACCTGGATGAAATGGCTTGGATTGCTCTCGAAAATGTTAATCTATGATCCAGCCA
AACGAATTCTGGCAAAATGGCACTGAATCATCCATATTTAATGATTGGACAATCAGA
TTAAGAAGATGTAGCTTCTGACAAAAAGTTCCATATGTTATGTCAACAGATAGTTGTG
TTTTATTGTTAACTCTGTCTATTTGCTTATATATTTCTTGTATCAAACCTTC
AGCTGTACTTCGTCTCTAATTTCAAAAATATAACTTAAAATGTAATATTCTATATGA
ATTTAAATATAATTCTGTAATGTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 2

MEDYTKIEKIGEGTYGVVYKGRHKTGQVVAMKKIRLESEEEGVPVSTAIREISLLKELRH
PNIVSLQDVLMQDSRLYLYFEFLSMDLKKYLDSSIPGQYMDSSLVKVVTLWYRSPEVLLG
SARYSTPVDIWSIGTIFAELATKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDY
KNTFPKWKPGSLASHVKNLDENGLLSSKMLIYDPAKRISGKMALNHPYFNDLDNQIKKM

cAMP- and cGMP-dependent protein kinase phosphorylation site.

217-220

Tyrosine kinase phosphorylation site.

9-15

N-myristoylation site.

27-32

43-48

134-139

164-169

190-195

Protein kinase domain
4-230

FIGURE 3A

CCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAATGGAAAAGTACCAACGTGTT
 GGAGATGATGGAGAAGGCTCTTTGGGAGGGTGTACAAGGGTCAAGAAAATACAGTGC
 TCAGGTCTGGCCCTGAAGTTCATCCAAAATTGGGGCGCTCAGAGAAGGAGCTGAGGAA
 TTTGCAACGAGAGATTGAAATAATGCGGGTCTGCGGCATCCACATTGTGCATATGCT
 TGACAGCTTGAAACTGATAAAGAGGTGGTGGTGGTGTACAAGACTATGCTGAGGGAGAGCT
 CTTTCAGATCCTAGAAGATGACGAAAACCTCCTGAAGACCAGGGTCAAGGCATTGCTGC
 CCAGTTGGTGTCAAGCCCTGTACTATCTGCATTCCACCGCATCACCAGAGATATGAA
 GCCTCAGAACATCCTCTCGCCAAGGGTGGTGGCATCAAGCTCTGTGACTTTGGATTG
 CCGGGCTATGAGCACCAATAACATGGTGTGACATCCATAAAGGCACACCACTCTATAT
 GTCTCAGAGCTGGTGGAGGAGCACCATAACGACCACACAGCGGACCTCTGGTCTGTTGG
 CTGCATACTATATGAACTGGCAGTAGGCACCCCTCCCTCTATGCTACAAGCATCTTCA
 GCTGGTCAGCCTCATTCCTCAAGGACCTGTGCGCTGGGCTCAACCATCAGTCCCTGCTT
 TAAGAACTTCCTGAGGGACTGCTCACCAAGACCCACGGCAGCAGCTGTCTGGCCAGA
 CCTCTTATATCACCCCTTATTGCTGGTCATGTCACCATAATAACTGAGCCAGCAGGCC
 AGATTGGGGACCCATTCAACCAGCCCTACCCCCAGAACTTCAGGTCTAAAGGACGA
 ACAGGCCATCGGTTGGCCCCAAGGTAATCAGTCTCGCATCTGACTCAGGCCTATAA
 ACGCATGGCTGAGGAGGCCATGAGAACATCAGAACACAGGACCTGCCCTGAGCA
 AGAGGACAAGACCAGCAAGGTGGCTCTGGCACAGCCCTCTGCCAGACTCGGGGCCAC
 TCCTCAGGAATCAAGCCTCTGGCCGGATCTTAGCCTCAGAATTGAAGAGCAGCTGGGC
 TAAATCAGGACTGGAGAGGTGGCTCTGCACTCGGAAACCCAGGACCTGCCAGATTTG
 TGAACGAGCATTCCAGAGGAGAGGCCAGAGGTGCTGGCCAGGGAGCAGTGTAGT
 GGACCTGGAAAATGAGGAGGCCAGACAGTGACAATGAGTGGCAGCACCTGCTAGAGACCAC
 TGAGCCTGTGCCTATTCAACTGAAGGCTCTCACCTGCTGTAATCCTGACTTCTG
 CCAGCGCATCCAGAGTCAGCTGCATGAAGCTGGAGGGCAGATCTGAAAGGCATCTGGA
 GGGTGCCTCCACATCCTGCCTGCATTCCGGGCTCTGAGCAGTCTCTCTCAGCTGCAG
 TGATTCTGTTGCCTGTATTCCCTCTGCCGGGAGGCAGGGCTCTGGCTGCTGCTGAG
 TCTACTCAGGCACAGTCAGGAGAGCAACAGCCTCCAGCAGCAACTTGGTATGGGACCTT
 CTTACAGGACCTGATGGCTGTGATTCAAGGCTACTTTGCCTGTAACCTTCAACTCTGGAGAG
 GAGCCAGACAAGTGACAGCCTGCAGGTGTTAGGAGGCTGCCAACCTTTCTGGACCT
 GTTGGGAAACTGCTGGCCAAACAGATGACTCTGAGCAGACTTGCAGGAGCAGCT
 TATGTGCTTACTGCTCTGTGCAAGCCATGGATGGGAAACAGCCGGCCATCTCAAAGC
 CTTTACTCCAGCTGCTGACGACACAGCAGGTTGCTGGATGGGCTCCTCATGGCTT
 GACAGTTCCACAGCTCCCTGTCCACACTCCCCAAGGAGCCCTGCCAGTGAAGCCAGCCACT
 GCGAGAGCAGAGTGAGGATACCTGGAGCCATTCCCTGCCCCAGCCATATGCAC
 TGCTCCGTGGACTGCCGACTGCTGGGATGCCAAGGAGCAGGTCTGTTGCCATTGGC
 AAATCAGCTAATGAAAGACAGCAGCCAGCTCAGGCCATCCCTCATCTGCTGCAGCA
 TCCCATCCTGTGCCTGCACCTCTCAAGGTCTATACCTCTGCTGCCTTGTCAGTGAGGG
 CCTGTGCCGTCTCTGGGAGCCCTGGCTTGGAAATCCCTGTTATGTTGATTCA
 GGGCAAGGAAAAGTAGTGTAGATTGGGAAAGACTCTACTGAAGTGACACTCTACTCCCTC
 CCTTCTGTCTTCCGCTCCAAAACCTGCCCTGTGGAATGGAGAAGCTAGGCAGTGACGT
 TGCTACTCTCTTACCCATTGCGATGTCGCTCTCTTGAGTGACTGAGCAGCCTGTCTATT
 GGGACAGCTGGTCAGCAAGGGGTGACCTTGACCTCCAGCCATGGAATGGATGGCTG
 AGCCACACATGCCCTGTCTGCCCTGAGAGGTTGGTGAETCCACCAGGTAGTTGTGG
 ATTCTATGATGCCCTCTTATCCTCTGTTGAGCTCCTCACTGAGCAGGGAGGGCTAG
 CCTAATCAGGGATATGTCAGTCAGAAATGTTGGACCGTTTGTCAGGCCCTCTCCAT
 GGTCTGAGGCTCCCCAGGGAGGCATCTGCACAGGAAGGGAGCTTCGCTATCCAGTCC
 ACCAAGCCCTGAGCCAGACTGGACACTGATTCTCCAGGGCATGGCAGCCCTGCTGAG
 CCTGGCCATGCCACCTTACCCAGGAGCCCTAGTTATGCCCTGAGCTGCCCTGCTGCCAGCA
 TGGAAAGTATCCTCATGTCCTGAGACATCTGCTCTGCTTGGCCCAAGCTTCTGAAATCAACT
 GCGCCAGGGCCTCATGGGCTGAGTTCTCCCTGTCGTTGGTGTCTCTGCTGCCAGCT
 CCTTGCTCCCCCTTGGCCTGGACATGGATGCTGACCTCCCTTATAGTTGTCTGGCCGA
 CCTCAGGGACTCAGAAGTTGCAAGCCATCTGCTGAGGTCTGCTGCTACCATCTCCGTT
 GATGCAAGTGGAGCTGCCCATCAGCCTCTCACACGCCCTGGCCCTCATGGATCCCACCTC
 TCTCAACCAGTTGAGACACAGTGCTGCCCTCCCTAGAACCATGTCCTGTTCTCTC
 AGTTGCCCTCTGAGTGACAGGCCACTGTTGACCTCCGACCTCTCTCTGCTGGCCA
 TACTGCCAGGGCTCTGTCTCCAGCCACTTGTCTTATCCAAGAGCTCTGGCTGGCTC
 TGATGAATCCTATGCCCTCTGCCAGCCTCCCTGGCCACCCAGAGAATTGTCGCGGGC
 ACACACTTATAGGCTCTGGGACACTTGCTCCAACACAGCATGCCCTGCCCTGGGGCACT
 GCAGAGGCCAGTCTGGACTGCTCAGCCTCTGCTGCTGCTGGGCTGGAGACAAGGATCCTGT
 TGTGCGGGTGCAGTGCAGCTTGTGCTGGGCAATGCAAGCTACCCAGGCTGGCCTCTGG
 ACCTGCCCTGGCAGCTGCAGTGCCAGTACGACCCAGCTGCTGGAGATCCTCAGGCTGG
 TATCCGGCGCAATGTCATCAGCTGGCAACTTGGGACCTGAAGGTTGGGAGAGGA

FIGURE 3B

GCTGTTACAGTGCAGTACCCAGCGGCTCTAGAAATGGCATGTGGAGACCCCCAGCC
AAATGTGAAGGAGGCTGCCCTCATGCCCTCCGGAGCCTGCAACAGGAGCCTGGCATCCA
TCAGGTACTGGTGTCCCTGGGTGCCAGTGAGAAAATACCTTGCTCTCTGGGAATCA
GTCACTGCCACACAGCAGTCCTAGGCCTGCCAACACTGCAGGAAACTCATTCA
CCTCCTGAGGCCAGCCATAGCATGTGAAAGCTTGGCCGCCATGGCCC

FIGURE 4A

MEKYHVLEMIGEGSFGRVYKGRRKYSQQVALKFIPKLGRSEKELRNLQREIEIMRGLRH
 PNIVHMLDSFETDKEVVVTDYAEGELFQILEDDGKLPEDQVQAIQAAQLVSALYLYLHSRH
 ILHRDMKPQNILLAKGGGIKLCDFGFARAMSTNTMVLTSIKGTPLYMSPELVEERPYDHT
 ADLWSVGCILYELAVGTPPFYATSIFQLVSLILKDPVRWPSTISPCFKNFLQGLLTKDPR
 QRLSWPDLLYHPFIAGHVIIITEPAGPDLGTPFTSRLPPELQVLKDEQAHRLAPKGNQSR
 ILTQAYKRMAEEAMQKHQNTGPALQEDKTSKVAPGTAPLPRLGATPQESSLLAGILAS
 ELKSSWAKSGTGEVPSAPRENRTPDCEARFPEERPEVLGQRSTDVVVDLENEEPDSDNEW
 QHLLETTPEVPIQLKAPLTLNCDFCQRIQLHEAGGQILKGILEGASHILPAFRVLS
 SLLSSCSDSVALYSFCREAGLPGLLSLLRHSQESNSLQQQSWYGTFLQDLMAVIQAYFA
 CTFNLERSQTSDSLQVFQEAANLFLLGGKLLAQPDDEQTLRRDSLMCFTVLCEAMDGN
 SRAISKAFYSSLLTQQVVLGGLHGLTVPQLPVHTPQGAPQVSQPLREQSEDIPGAISS
 ALAAIACTAPVGLPDCWDAKEQVCWHLANQLTEDSSQLRPSLISGLQHPILCLHLLKVLYS
 CCLVSEGLCRLLGQEPLAELSFMLIQQGKVVVDWEESTEVTLYFLSLLVFRQLQNLPCGM
 EKLGSDVATLFTSHVVSLSVAAACLLGQLGQGVTFDLQPMEMAAATHALSAPAEVRL
 TPPGSCGFYDGLLLQLTEQGKASLIRDMSSEMWTVLWHRFSMVLRLPEEASAQEG
 ELSLSSPPSPEPDWTLISPQGMAALLSLAMATFTQEPQLCISLQHGSILMSILKHL
 PSFLNQLRQAPHGSEFLPVVVLSVCQLLCFFALDMADLLIVVLADLRSEVAHLLQV
 CCYHPLMQLMQLPISLLTRLALMDPTSLNQFVNTVSASPRIVSFLSALLSDQPLLTSD
 LLSLLAHTARVLSPLSHLSFIQEILLAGSDESYRPLRSLIGHPENSVRAHTYRLLGHLLQHS
 MAIRGALQSQSGLLSLLGLGDKDPVVRCASFAGVNAAYQAGPLGPALAAAVPSMTQL
 LGDPQAGIRRNVASALGNLGPEGLGEELLQCEVPQRLLEMACGDPQPNVKEAALIALRSL
 QQEPMIHQVLVSLGASEKLSLLSLGNQSLPHSSPRPASAKHCRKLIHLRPAHSM

N-glycosylation site.

297-300
 381-384
 1286-1289

Glycosaminoglycan attachment site.

369-372

cAMP- and cGMP-dependent protein kinase phosphorylation site.

23-26
 583-586

N-myristoylation site.

138-143
 270-275
 356-361
 400-405
 464-469
 503-508
 599-604
 622-627
 656-661
 671-676
 784-789
 1106-1111
 1145-1150
 1207-1212

Amidation site.

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FIGURE 4B

Leucine zipper pattern.

769-790
987-1008

Serine/Threonine protein kinases active-site signature.

121-133

Protein kinase domain
1-294

FIGURE 5A

CAGAGCGAGGGCGAGAGCCGATCAGCGGATCACCGAGTCTCGCCAGGTGGTGGAGCTGGCA
 GTGAAGGAGCACAAGGCTGAGATTCTGCTCTGCAGCAGGCTCTAAAGAGCAGAAGCTG
 AAGGCCGAGAGCCTCTGACAAGCTCAATGACCTGGAGAAGAAGCATGCTATGCTTGA
 ATGAATGCCCGAAGCTACAGCAGAAGCTGGAGACTGAACGAGAGCTCAAACAGAGGCTT
 CTGGAAGAGCAAGCCAATTACAGCAGCAGATGGACCTGCAGAAAAATCACATTCCGT
 CTGACTCAAGGACTGCAAGAAGCTAGATCGGGCTGATCTACTGAAGACAGAAAGAAGT
 GACTTGGAGTATCAGCTGGAAAACATTCAAGGTTCTTATTCTCATGAAAAGGTGAAAATG
 GAAGGCACTATTCTCAACAAACCAACTCATTGATTCTGCAAGCAAAATGGACCAA
 CCTGCTAAAAAGAAAAGGTTCTCTGCAGTACAATGAGCTGAAGCTGGCCCTGGAGAAG
 GAGAAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTCAGAAGACCCGCATCGAGCTCCGG
 TCCGCCCGGGAGGAAGCTGCCACCGCAAAGCAACGGACCACCCACACCCATCCACGCCA
 GCCACCGCGAGGCAGCAGATGCCATGTCGCCATCGCGTCCAGAGCACCAGGCC
 AGTGCATGAGCTGTCGGCCATCCAGCGCAGAAAGGAGTCTCAACTCCAGAG
 GAATTAGTCGGCTCTTAAGGAACGCAGCACCACAAATTCCTCACCGATTCAACGTA
 GGACTGAACATGCGAGGCCAAAGTGTGCTGTGCTGGATACCGTGCACTTGGACGC
 CAGGCATCCAAATGTCGAAATGTCAGGTGATGTGTCACCCCAAGTGTCCACGTGCTG
 CCAGCCACCTGCGGCTGCCGTGTAATATGCCACACACTCACCGAGGCCCTCTGCCGT
 GACAAAATGAACTCCCAGGTCTCAGACCAAGGAGCCAGCAGCAGCTGCCACCTGGAA
 GGGTGGATGAAAGGTGCCAGGAATAACAAACGAGGACAGCAAGGCTGGGACAGGAAGTAC
 ATTGTCCTGGAGGGATCAAAAGTCCTATTATGACAATGAAGCCAGAGAAAGCTGGACAG
 AGGCCGGTGGAGAATTGAGCTGTGCCTTCCGACGGGATGTATCTATTATGAGTGG
 GTTGGTGCTCCGAACCTCGAAATACAGCAAAGCAGATGTCCCATACATACTGAAGATG
 GAATCTCACCGCACACCCACTGCTGGCCCGGAGAACCCCTACTGCTAGCTCCAGC
 TTCCCTGACAAACAGCGCTGGGTCACCGCCTTAGAATCAGTTGCTGCAGGTGGAGAGTT
 TCTAGGGAAAAGCAGAAGCTGATGCTAAACTGCTTGGAAACTCCCTGCTGAAACTGGAA
 GGTGATGACCGTCTAGACATGAAACTGCAACCGCTGCCCTCAGTGACCAAGGTGGTGG
 GGCACCGAGGAAGGGCTCTACGCCCTGAATGTTGAAAACCTCCAAACCATGTCCA
 GGAATTGGAGCAGTCTCCAAATTATATTCAAGGACCTGGAGAAGACTACTCATGATA
 GCAGGAGAAGAGCGGGCACTGTCCTGGACGTGAAGAAAGTGAACAGTCCCTGGCC
 CAGTCCCACCTGCCCTGCCAGCCGACATCTCACCCAAACATTGAGTGTCAAGGGC
 TGCCACTTGGGGCAGGCAAGATTGAGAACGGGCTCTGCATCTGTGCAGCCATGCC
 AGCAAAGTCGTCAATTCCGCTACAAACGAAAACCTCAGCAAATACTGCATCCGAAAGAG
 ATAGAGACCTCAGAGCCCTGCAGCTGTATCCACTTCACCAATTACAGTATCCTCATTGGA
 ACCAATAAAATTCTACGAAATCGACATGAAGCAGTACACGCTCGAGGAATTCTGGATAAG
 ATAGACCATCCTGGCACCTGCTGTTGCGCCTCTTCAACAGCTTCCCTGTC
 ATCGTGCAGGTGAAACAGCGCAGGGCAGCAGGAGAGTACTTGCTGTGTTCCACGAATT
 GGAGTGTGCGGATTCTTACGGAAGACGTAGCCGCACAGACGATCTCAAGTGGAGTC
 TTACCTTGGCCTTGCCTACAGAGAACCCATCTGTTGACCCACTCAACTCACTC
 GAAGTAATTGAGATCCAGGCACGCTCCTCAGCAGGGACCCCTGCCGAGCGTACCTGGAC
 ATCCCGAACCGCGCTACCTGGGCCCTGCCATTCTCAGGAGCGATTACTTGGCGTCC
 TCATACCAGGATAAAATTAAAGGGTCAATTGCTGCAAGGGAAACCTCGTGAAGGAGTC
 ACTGAACACCACCGGGCCGTCACCTCCCGCAGCAGCCCAAACAGCGAGGCCACCC
 ACGTACAACGAGCACATACCAAGCGCGTGGCCTCCAGCCAGGCCAGGCCAGGCC
 AGCCACCCCGAGAGCCAAGCACACCCACCGCTACCGGAGGGCGGAGCGTCC
 AGGGACAAGTCTCTGGCCGCCCTGGAGCAGAGAAGTCCCCGGCGATGCTCAGC
 ACGCCGGAGAGAGCGGTCCCCCGGGAGGCTGTTGAAGACAGCAGCAGGGCGGCTGCC
 CGGGAGCGGTGAGGAGCCCCGCTGTCCTCAGGTGAACAAGGTCTGGGACCAGTCTCAGTA
AAAATCTCAGCCAGAAAACCAACTCCTCATCTGATCTGCAGGAAAACACCAACACAC
 TATGGAACACTGCTGATGGGGACCCAAGGCCACGTGCTAGCCACCCCTCTGGCTCAGC
 GGGGCCAGACCCACCTCGGCACGGACACCCCTGTCTCCAGGAGGGCAGGTGGCTGAGG
 CTCTCGGAGCTGTCAGCGCCGGTGCCTGCCCTGGCACCTCCCTGCACTCATCTT
 GCACATTGTTACTCTTCAAGCATTACAAACTTTGTACCTAGCTAGCCTGTACCA
 GTTAGTTCATCAAAGGAAACCAACCGGGATGCTAACAAACACATGGTTAGAATCTAAATT
 AGCTACTTAAGATCCTAGGATTGGTTGGTTTTCTTTTTCTCTTTGTTCTTTC
 CTTTTTTTTTTTTTTAAGACAACAGAAATTCTTAATAGATTGAATAGCGACGTATT
 TCCTGTTGTTAGCTGACCGACCATCATCAGGTCTTGCCACCGAGGCATAGT
 GTAGAACAGTCCCGTCACTGGCCAACCTCCCGCAGCCAAGTAGGTTCATCCTTGT
 TGTTGTTAGCTGCTTGTGACGACTCCCTCCACCGACTGAGAATGTATGGA
 GGTCACTGGGGCCTCAGCTGGAGGCAGTGACTGGGGCCAAGGGACCTCGAGACGCTT
 CCTCCCCACCCCCCAGCGTCACTCCCCCAGCCTGCTGTTCCGCTTCCATATAGCTT
 GGCCAGGAAAGCATGCAATAGACTTGCTGGAGCCCAGCACTCCTGGGTCTCGGGTC
 GGG

FIGURE 5B

GGAGGGGACGGGGGACCCACTTCTTGTGACGGCGTGTGTTCCCCACTCTGGGA
TGGGAAGAGGCCGTCGGAGTTCTGCATGGCAGTTCACTGCATGTGCTGCCCCCTTGG
GTGCTCTGCCAATGTATTAATACCATCCCAGCTCTGCCAAATCGAGACCCCTGTGAC
GAATTGCCACTAAGCTGAGGACCCACAAGCTGCAGTCTGAGCAACTGAACAAACAAAAAC
AAAACGCTCAAGCCTAACGACCAAGAGGATTTCAGCAAACCCACCTCCACTCAGT
GTCCCCCTCCAAACTTCACACTTCCCTGCCTGCAGAGGACTCTGTTCACACCCAAATCC
AGCGCGGTTCTACCCCCACGAAACTGTGACTTTCCAAATGAGCCTTCCCTAGGGCTAGAC
CTAAGACCAAGGAAGTTGAGAAAGCAGCCGAGCTCAACTCTTCAGCTCCGCCAGGGTT
GGGAAGTCCTTAGGTGCAGTGCAGCTCCACTGGGTCTGCAGGACCCCTATTAGAGTAC
GAAATTCTGGCAACTGGTATAGAACCAACCTAGAGGCTTGCAGTTGGCAAGCTAAC
GCAGCCCTATTCTGCCTTAATCTCCCACAGGCATCTGTTGCTTGGGTCTCCACGA
CTCTTAGGCCCGCCTCAACAACCCAGGCACCTCTAGTAGGCTAAAGGTAGACCCGTT
TCCACCGCAGCAGGTGAACATGACCGTGTCTCAACTGTGTCACAGTTCAAGATCCCTT
CCAGATTGCAACCTGGCCTGCATCCCAGCTCCTCTGCTGCTCTTAACCTAAC
TTCTGTTGAAACGCTACAAACCTCATGGTAGCTCTGGCAAATGTCTGCTG
TGGCGTTTATGTGTTGCTGGAGCTGTGTTGGGTCTGACTCCCTCCCGTCCCCAG
GGCAGATTGATTGAAATGTTGCTGAAGTTGCTCTGGTCCACAGTATTGGAAAGG
TCACTGAAATGGGTCTTCAGTCTGGCATTTCATTAGGATCTCCATGAGAAATGGGC
TTCTTGAGCCCTGAAAATGTATATTGTGTTGCTCATCTGTGAACTGCTTCTGCTATATA
GAACTAGCTCAAAAGACTGTACATATTTACAAGAAACTTATATTCTGAAAAAAAG
AGGAAATTGAATTGGTTCTACTTTTATTGTAAGGTGCATTTCAACACTTACCT
TTGGTTTCAATGGTGGTAGTTGTTGACAGCCATCTCACTGGAGGGTGGGAGCTCCGTG
TGACCACCAAGATGCCAGCAGGATATACCGTAACACGAAATTGCTGTCAAAGCTTATA
GCATCAATCAAGATTCTAGGTCTCCAAAAGTACAGGGCTTTCTCATTACCTTTTAT
TCAGAACGAGGAAGAGAACACAAGGAATGATTCAAGATCCACCTTGAGAGGAATGAACCT
TGTTGTTGAACAATTAGTGAATAAGCAATGATCTAAACT

9/46

FIGURE 6

MLEMNARSLQQKLETERELKQRLLEEQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKT
ERSDLEYQLENIQVLYSHEKVKGMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLA
LEKEKARCAELEEALQKTRIELRSAREEAAHRKATDHPHPSTPATARQOIAMSAIVRSPE
HQPSAMSLIAPPSSRRKESSTPEEFSSRRLKERMHHNIPHRFNVGLNMRAVKCAVCLDTVH
FGRQASKCIECQVMC PKCSTCLPATCGLPAEYATHFTEAFCRDKMNSPGLQTKEPSSSL
HLEGWMKVPRNNNKRGQQGWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSI
HGAVGASELAAKADAVPYIILKME SHPHTTCWPGRTLYLLAPSFPDKQRWVTALESVVA
GRVSREKAEDAKLLGN SLLKLEGDDRLLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLT
HVPGIGAVFOIYIYIKDLEKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI
VKGCHLFGAGKIEENG CICAAMPSKV VILRYNENLSKYCIRKEIETSEPCSCI
HFTNYSI LIGTNKFYEIDMKQY TLEELDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQ
RE EYLLCF HEFGFVFDSYGRRSRTDDLKWSRLPLAFAYREP YLFVTHFNSLEVIE
IQARSSAGTPARA YLDIPNPRYLGPAI SSGAIYI LASSYQDKLRVICCKGNLV
KESGT EHHRGPSHSRSPNKR GPPTYNEHITKRVASSPAPPEGPSH
PREPSTPHRYREGRTELRRDKSPGRPLEREKSPGR
MLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVWDQSSV

N-glycosylation site.

451-454
574-577
597-600

cAMP- and cGMP-dependent protein kinase phosphorylation site.

152-155
196-199

N-myristoylation site.

47-52
362-367
420-425
464-469
555-560

Amidation site.

670-673

Carbamoyl-phosphate synthase subdomain signature 2.

1-8

CNH domain
448-745

PH domain
300-419

Phorbol esters/diacylglycerol binding domain
219-267

10/46

FIGURE 7

AAAGGCCTGCAGCAGGACGAGGACCTGAGCCAGGAATGCAGGATGGCGGCGGTGAAGAAG
 GAAGGGGGTGCCTCTGAGTGAAGCCATGTCCTGGAGGGAGATGAATGGGAACGTGAGTAAA
 GAAAATGTACAACCTTAAGGCAAGGGCGATCATGTCCACGCTTCAGGGAGCACTGGCA
 CAAGAATCTGCCTGTAACAATACTCTTCAGCAGCAGAAACGGGCATTGAATATGAAATT
 CGATTTACACTGGAAATGACCCCTGAGTTGGGATAGGTATATCAGCTGGACAGAG
 CAGAACTATCCTCAAGGTGGGAAAGAGAGTAATATGTCAACGTTATTAGAAAGAGCTGTA
 GAAGCACTACAAGGAGAAAAACGATATTATAGTGTACCTCGATTTCATCTGGCTT
 AAATTAGGGCGTTATGCAATGAGCCTTGGATATGTACAGTTACTTGCAACAACCAAGGG
 ATGGTGTTCACTTGCTCAGTTCTATATCTCATGGGCAGAAGAAATATGAAGCTAGAGAA
 AACTTAGGAAAGCAGATGCGATATTCAGGAAGGGATTCAACAGAAGGCTGAACCACTA
 GAAAGACTACAGTCCCAGCACCGACAATTCCAAGCTCGAGTGTCTGGCAAACCTGTGTT
 GCACCTGAGAAAGAAGAGGAGAAGTTTGAGTCTCTGTACCCACAAGCAAGCACA
 CTAGCTGAACAAAGAGCAAAGGGAAAAGACAGCAAGAGCTCCAAATCATCCGTGTAGGA
 GGTGCTCTCAAGGCTCCAAGGCAGAACAGAGGACTCCAAAATCCATTCTCAACAGATG
 CAAAATAATAGTAACTACTGTTTGATGAAAATGCTGATGAGGCTTCTACAGCAGAG
 TTGCTTAAGGCTACAGTCCAGGCCATGGAGCACCCCCATGCCAGGGCCAAGAGAAAT
 GAGCTGCAAGCAGGCCCTTGGAACACAGGAGCTGTGCTTCCAGTTCACTCATATGTGGAAGAG
 ACTGCACAACAGCCAGTTATGACACCATGTAATTGAAACCTAGTATAAACACATCCTA
 AGCACCAGAAAGCCTGGAAAGGAAGAAGGAGATCCTCTACAAAGGGTTCAGAGCCATCAG
 CAAGCGCTGAGGAGAAGAAAGAGATGATGTTGTAAGGAGAAGATTATGAGGA
 GTAGGGAAATTCTCCTTGAAGAAATTGCGGCTGAAGTTTCCGGAAGAAATTAAAGAG
 CAAAGGGAAAGCCGAGCTATTGACCAAGTGCAAGAGAAGAGAGCAGAAATGCAGAAACAGATT
 GAAGAGATGGAGAAGAAGCTAAAAGAAATCCAAACTACTCAGCAAGAAAGAACAGGTGAT
 CAGCAAGAAGAGACGATGCCCTACAAAGGAGACAACAAACTGCAAATTGCTCCGAGTCT
 CAGAAAATACAGGAATGACTCTATCCAGTTCTGTTGTCAGTAAACTGTTGTGCCAGA
 GAAACTTCACTTGCGGAGAACATTGGCAGGAACAACCTCATTCTAAAGGTCCCAGTGT
 CCTTCTCCATTGGATGAGTTCTTCTTCAGAAAAGAAGATAAAAGTCTCTGCA
 GATCCCCACGAGTTAGCTCAACGAAGACCCCTGCAAGTTCTCAAAACCTCAGAAAGC
 ATCACCTCAAATGAAGATGTCCTCAGATGTTGATGAATTACAGGAATTGAACCC
 TTGAGCGAGGATGCCATTATCACAGGCTTCAGAAATGTAACAATTGTCCTAACCCAGAA
 GACACTTGTGACTTGCAGAGCAGCTCGTTGTATCCACTCCTTTCATGAGATAATG
 TCCCTGAAGGATCTCCCTCTGATCCTGAGAGACTGTTACCGGAAGAAGATCTAGATGTA
 AAGACCTCTGAGGACCAGCAGACAGCTGTCGCACTATCACAGTCAGACTCTCAGCATC
 AAGAAGCTGAGCCAAATTGAGACAGCTCGTGAAGGCACACACTCCTCTGCTTCTCT
 GGTTCTCTGCTCGGTTGCAAGCACCCTCCATCAAATGTCCTAAATCTGAGAA
 CTAGAACTTACTAATGAGACTTCAGAAAACCTACTCAGTCACCATGGTGTACAGTAT
 CGCAGACAGCTACTGAAGTCCCTACCAGAGTTAAGTGCTCTGCAAGAGTTGTATAGAA
 GACAGACCAATGCCAAAGTGGAAATTGAGAAGGAATTGAAATTAGGTAATGAGGATTAC
 TGCATTAAACGAGAACACTAATATGTGAAGATTACAAGTTATTCTGGGTGGGCCAAGA
 AACTCTGCAGAATTAAACAGTAATAAAAGGTATCTCTAACCTGTCCCATGGACTTTAT
 ATCAACCTCAAGTTAAAGGAACGTTAAATGAAGATTGATCATTGCAAGCTGTTAT
 CAATATCAAGATGGCTGATTGTTGGCACCAATATAAAACTGCTTCACCCCTCAGGAT
 CTTCTCCAAACACAGTGAATATTACCCATGAAATAACAGTGTGATTATTATAACCTT
 TTGACAATAGTGGAGATGCTACACAAAGCAGAAATAGTCCATGGTACTGAGTCCAAGG
 TGTCTGATTCTCAGAACACAGAACATCCACGATCCCTATGATTGTAACAAGAACAAATCAAGCT
 TTGAAGATAGTGGACTTTCCCTACAGTGTGACCTTAGGGTCAGCTGGATGTTTAC
 CTCAGCGGTTTCCGACTGTACAGATCCTGGAAGGACAAAAGATCCTGGCTAAGTGT
 TCTCCCTACCAAGGTAGACCTGTTGGTATAGCAGATTAGCACATTACTATTGTCAG
 GAACACCTACAGGTCTCTGGATGGTCCTCTGGAACACTTAGCAGAAATTTCTGAG
 CTAAAAGATGGTAATTGGAATAAAATTCTTGTGCGGATTCTGAATGCCAATGAG
 GCCACAGTGTCTGTTCTGGGGAGCTGCAAGCAGAAATGAATGGGTTTGACACTACA
 TTCCAAAGTCACCTGAACAAAGCCTTATGGAAGGTAGGAAAGTTAAGTACTAGTC
 TTGCTCTTCAGTCAGCTAGGCAATCAAGTCACAGATTGCTGCTCAGAGCAATGGTT
 GTATTGTGGAACACTGAAACTGTATGTGCTGTAATTAAATTAGGACACATTAGATGCA
 CTACCATGCTGTTCTTGTACAGGTATTTGACGTACTGATAATTGTTAT
 ACAGTGTATATCTTACTCTTGTACAGGTTATTGAGAAGAACTATTGTTATTCTAA
 CAGACTCATTACAAATGGTACCTGTTATTAAACCCATTGTCCTACTTTCCCTGTA
 CTTTCCCATTTGTAATTGTAATTGTTCTTATGATCACCATGTTATTGTAATAA
 TAAAATAGTATCTGTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 8

MAAVKKEGGALSEAMSLEGDEWELSKENVQPLRQGRIMSTLQGALAQESACNNTLQQQKR
 AFYEYEIRFYTGNDPLDVWDRYISWTEQNYPQGGKESNMSTLLERAVEALOGEKRYYS DPR
 FLNLWLKLGLRCNEPLDMYSYLHNQGIGVSLAQFYISWAEEYEARENFRKADAIFQEGIQ
 QKAEPLERLQSQHRQFQARVSROTLLALEKEEEEVEFESSVPQRSTLAEKSKGKKTARA
 PIIRVGGALKAPSQNRLQNPFPQQMNNSRITVFDENADEASTAELSKPTVQPWIAPP
 PRAKENELQAGPWNTRGSLEHRPRGNATSLIAVPAVLPSFTPYVEETAQQPVMTPCKIEP
 SINHILSTRKPGKEEGDPLQVRQSHQQAEEKKMCKEKIYAGVGEFSFEEIRAEVF
 RKKLKEQREAEELLTSAEKRAEMQKQIEEMEKKLKEIQTQQERTGDQQEETMPTKETTKL
 QIASESQKIPGMLLSSSVQVNCCARETSLAENIWOEQPHSKGPSVPFSIFDEFLLSEKK
 NKSPPADPPRVLQAQRRPLAVLKTSSESITSNEDVSPDVCDEFTGIEPLSEDAAITGFRNVT
 ICPNPEDTCDFAARAARFVSTPFHEIMSLKDLPSDPERLLPEEDLDVKTSEDQQTACGTIY
 SQTLSIKLSPPIEDSREATHSSGFSGSSASVASTSSIKCLQIPEKLELTNETSENPTQS
 PWCSQYRRQLLKSPELSSAELCIEDRPMPLKIEKEIELGNEDCYIKREYLICEDYKL
 FWVAPRNSAELTVIKVSSQPVPDFYINLKLKERLNEDFDHFCSCYQYQDGCIIVWHQYIN
 CFTLQDLLQHSEYITTHEITVLIYNNLTIVEMLHKAЕIVHGDLSPRCLILRNRIHDPYDC
 NKNNQALKIVDFSYSVDLRVQLDFTLSGFRTVQILEGQKILANCSSPYQVDLFGIADLA
 HLLLFFKEHLQVFWDGFWKLSQNISELKDGELWNKFFVRILNANDEATVSVLGEAAEMN
 GVFDTTFQSHLNKALWKVGKLTSPGALLFQ

N-glycosylation site.

52-55
 97-100
 268-271
 598-601
 711-714
 944-947
 983-986

cAMP- and cGMP-dependent protein kinase phosphorylation site.

667-670

Tyrosine kinase phosphorylation site.

908-914

N-myristoylation site.

8-13
 92-97
 146-151
 148-153
 325-330
 491-496
 657-662
 687-692
 1021-1026

Amidation site.

233-236

FIGURE 9

GGAAGACTTGGGTCTTGGTCGCAGGTGGGAGCCGACGGGTGGGTAGACCGTGGGGAT
ATCTCAGTGGCGGACGAGGACGGCGGGACAAGGGCGGCTGGTCGGAGTGGCGAGCGT
CAAGTCCCTGCGGTCTCTCCGCTCCTGGGACCGAGGCGCCCTGAGGATACTGCTTGTACTTAT
GCGCCTTGACATCCGCTCCTGGGACCGAGGCGCCCTGAGGATACTGCTTGTACTTAT
TACAGCTAGAGGCATCATGGACCGATCTAAAGAAAAGCTCAGGAACTGTTAAGGC
TACAGCTCCAGTGGAGGTCCAAAAGCTGTCTCGTGTACCTCAGGAACTTGTCAAGAA
TCCATTACCTGTAATAGTGGCCAGGCTCAGGGCTTGTGTCTTCAAATTCTCCA
GCGCGTCCCTTGCAGCACAAAAGCTGTCTCCAGTCACAAGCGGTTAGAATCAGAA
GCAGAAGCAATTGCAGGCAACCAGTGTACCTCATCCTGCTCCAGGCCACTGAATAACAC
CCAAAAGAGCAAGCAGCCCCGTCGCATCGGACCTGAAAATAATCCTGAGGAGGAACGGC
ATCAAAACAGAAAATGAAGAATCAAAAAGAGGCAGTGGGCTTGGAAAGACTTGAAT
TGGTCGCCCTCTGGTAAAGGAAAGTTGTAATGTTATTTGCAAGAGAAAAGCAAAG
CAAGTTTATCTGGCTCTAAAGTGTATTAAAGCTCAGCTGGAGAAAGCGGGAGTGG
GCATCAGCTCAGAAGAGAAGTAGAAATACAGTCCACCTCGGCATCCTAATATTCTTAG
ACTGTATGGTATTCATGATGCTACCGAGACTACCTAATTCTGGAATATGCACCACT
TGGAACAGTTATAGAGAACCTCAGAAAATTCAAAGTTGATGAGCAGAGAACTGCTAC
TTATATAACAGAATTGGCAATGCCCTGTCTTACTGTCATTGAGAGAGTATTGAGATT
AGACATTAAGGAGAGAACTTACTCTTGGATCAGCTGGAGAGCTTAAATGAGATT
TGGGTGGTCAGTACATGCTCCATCTCCAGGAGGACACTCTGTGGCACCTGGACTA
CCTGCCCTGAAATGATTGAAGGTGGATGCATGATGAGAAGGTGGATCTGGAGCCT
TGGAGTTCTTGCTATGAATTTTAGTTGGGAAGCCTCTTGAGGCAAACACATACCA
AGAGACCTACAAAAGAATATCACGGGTGAATTCACATTCCCTGACTTTGTAACAGAGGG
AGCCAGGGACCTCATTCAGACTGTTGAAGCATAATCCAGCCAGAGGCAATGCTCAG
AGAAGTACTGAACACCCCTGGATCACAGCAAATTCAAAACCATCAAATTGCCAAA
CAAAGAATCAGCTAGCAAACAGTCTAGGAATCGTCAGGGGAGAAATCCTTGAGCCAG
GGCTGCCATATAACCTGACAGGAACATGCTACTGAAAGTTATTTACCATTGACTGCTGC
CCTCAATCTAGAACGCTACACAAGAAATTTGTTTACTCAGCAGGTGTGCCCTAACCT
CCCTATTAGAACGCTCACATCAATAAACATGACACTCTGAAGTAAAGTAGCCACGAG
ATTGTGCTACTTATACTGGTTCATATCTGGAGGCAAGGTTGACTGCAGCCGCCCGT
CAGCCTGTGCTAGGCATGGTGTCTCACAGGAGGCAAATCCAGAGCCTGGCTGTGGGAA
AGTGACCACTCTGCCCTGACCCGATCAGTTAAGGAGCTGTGCAATAACCTTCCTAGTAC
CTGAGTGAGTGTAACTTATTGGTTGGCGAAGCCTGGTAAAGCTGTTGAATGAGTAT
GTGATTCTTTAAGTATGAAAATAAGATATATGTACAGACTTGTATTCTCTGTT
GGCATTCCCTTAGGAATGCTGTGTCTGCCGGCACCCGGTAGGCCTGATTGGGTTTC
TAGTCCTCCCTAACCACTTATCTCCCATATGAGAGTGTGAAAAATAAGGAACACGTGCTCT
ACCTCCATTAGGGATTGCTTGGGATACAGAAGAGGCCATGTGCTCAGAGCTGTTAAG
GGCTTATTAAAAACATTGGAGTCATAGCATGTGTAAACTTAAATATGCAAATA
ATAAGTATCTATGTCTAAAAAAAAAAAAAA

FIGURE 10

MDRSKENCISGPVKATAPVGGPKRVLVTQQIPCQNPLPVNSGQAQRVLCPSSQRVPLAQKLVSSHKPVQNQKQQLQATSVPHPSRPLNNTQSKQPLPSAPENNPEELASKQKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFAQLEKAGVEHQLRREVEIQSHLRHPNIRLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSKRVIHRDIKPENLLGSAGEELKIADFGWSVHAPSSRRTTLCGTLDDYLPPEMIEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTPDFVTEGARDLISRLKHNPSQRPMLREVLEHPWITANSSKPSCQNKEASKQS

N-glycosylation site.

52-55
93-96
386-389

cAMP- and cGMP-dependent protein kinase phosphorylation site.

285-288
339-342

Tyrosine kinase phosphorylation site.

326-334

Serine/Threonine protein kinases active-site signature.

252-264

Protein kinase domain
133-383

FIGURE 11

GGCGGGACAGTCCGCCGAGGTGCTCGGTGGAGTCATGGCAGTGCCCTTGTGGAAGACTGGACTTGGTCAAACCCCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTGCTGTGAATAGAGTAACGTGAAAGCAGTCGAGTGAAGATTGTAGATATGAAGCGTGCCTAGACTGTCCAGAAAATTTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCATGAAAATGTAGTAAATTCTATGGTCACAGGGAGAGAAGGCATATCCAATATTATTCAGGAGTACTGTAGTGGAGGAGAGCTTTTGACAGAAATAGAGCCAGACATAGGCATGCCCTGAACAGATGCTCAGAGATTCTTCCATCAACTCATGGCAGGGGTGGTTATCTGCATGGTATTGGAATACTCACAGGGATATTAAACCAAGAAAATCTTCTGGTGAAGGGATAACCTCAAATCTCAGACTTTGGCTTGGCAACAGTATTCGGTATAATAATCGTGAGCGTTGGTGAACAAGATGTGTGGTACTTACCATATGGCTCCAGAACTTCTGAAGAGAAAGAGAATTTCATGCAGAACCAAGTGTGTTGGCCTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGACCAACCCAGTGCAGCTGAGGAGTATTCTGACTGGAAAGAAAAAAACATACCTCAAACCTTGGAAAAAAATCGATTCTGCTCCTCTAGCTCTGCTGCATAAAATCTTAGTTGAGAACTCCATCAGCAAGAATTACCATCCAGACATCAAAAAGATAGATGGTACAACAAACCCCTCAAGAAAGGGCAAAAGGCCAGTCAGTCACTCAGGTGGTGTGTCAGAGTCTCCAGTGGATTTCAGCACATTCAATCCAAATTGGACTCTCTCCAGTAAACAGTGCTCTAGTGAAGAAAATGTGAAAGTACTCCAGTTCTCAGGCCAGAACCCGCACAGGTCTTCCTTATGGGATACCCAGCCCCTCATACATTGATAAAATTGGTACAAGGGATCAGCTTTCCAGGCCACATGTCCTGATCATATGCTTGAATAGTCAGTTACTGGCACCCCAAGGATCCTCACAGAACCCCTGGCAGCGGGTGGTCAAAAGAATGACACGATTCTTACCAAATTGGATGCAGACAAATCTTACATGCCTGAAAGAGACTTGTGAGAAGTTGGCTATCAATGGAAGAAAAGTTGTATGAATCAGGTTACTATCAACAACTGATAGGAGAAACAATAAAACTCATTTCAAAGTGAAATTGGTTAGAAATGGATGATAAAATTGGTGACTTCCGGCTTCTAAGGGTGATGGATTGGAGTCAGAGACACTCCTGAAGAGATTAAGGGAGCTGATTGATATTGTGAGCAGCCAAGAGTTGGCTTCCGACATGATCGGACCATCGGCCTGGGAATCCTGGTGAATATAGTCTGCTATGGACATTATTCTCCCTAGAGAAGATATCTGCTCTGCAAATGCAAATAGTAGTTCTGAAGTGTTCACTTCCCTGTTATCCAAACATCTCCAATTATTGGTTGTCGGCATACAAATAACCTATCTTAATTGTAAGCAAAACTTGGGAAAGGATGAATAGAATTCAATTGATTATTCCTCATGTTGTTAGTATCTGAATTGAAACTCATCTGGTGGAAACCAAGTTCAAGGGACATGAGTTCCAGCTTTACACACGTATCTCATTTTATCAAACATTGGT

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FIGURE 12

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINK
MLNHENVVKFYGHREGNIQYLFLEYCSGGELFDRIEPDGMPEPDAQRFFHQLMAGVY
LHGIGITHRDIKPENLLDERDNLKISDFGLATVFRYNNRERLINKMCGTLPYVAPELLK
RREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKTYLNPKWKKIDSAPLA
LLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKLVQGISFSQPTCPDHMLLNSQLL
GTPGSSQNFWQRLVKRMTRFFTLDADKSYQCLKETCEKLGYQWKKSCMNQVTISTTDRR
NNKLIFKVNLLEMDDKILVDFRLSKGDGLEFKRHFLKIKGKLIDIVSSQKVWLPAT

cAMP- and cGMP-dependent protein kinase phosphorylation site.

375-378

Tyrosine kinase phosphorylation site.

383-390
394-402

N-myristoylation site.

123-128
195-200
341-346
361-366

Serine/Threonine protein kinases active-site signature.

126-138

Protein kinase domain
9-265

FIGURE 13

CCGC GG TTCCGGCTGCTCCGGCGAGGCGACCCTGGTCGGCGCTGCGGGCGAGGTGGGC
AGGTAGGTGGCGGACGGCCGGTTCTCCGGCAAGCGCAGGCGGGAGTCCCCCACGG
CGCCCGAAGCGCCCCCGCACCCCGGCTCAGCGTTGAGGCAGGGAGTGAAGGAGATG
CCGACCCAGAGGGACAGCAGCACCATGTCCACACCGGTCGCAAGCGGGGGAGTGAAGGAGATG
CATTCCCACCAAGGTCCGGGTGAAAGCCTACTACCGCAGGGGGATATCATGATAAACACATT
GAACCTCCATCTCCTTGAGGGCCTTGCAATGAGGTTCGAGACATGTGTTCTTTGAC
AACGAACAGCTCTCACCATGAAAAGGATAGATGAGGAAGGAGACCGTGTACAGTATCA
TCTCAGTGGAGTTAGAAGAAGCCTTAGACTTTATGAGCTAAACAGGATTCTGAAC
TTGATTATGTGTTCCCTTGTGTACAGAACGTCCTGGGATGCCTGTCCAGGGAGAAGAT
AAATCCATCTACCGTAGAGGTGCAAGCCGCTGGAGAAAGCTTATTGTGCCAATGCCAC
ACTTCCAAGCCAAGCGTTCAACAGGCGTGCCTACTGTGCCATCTGCACAGACCGAATA
TGGGGACTTGGACGCCAAGGATATAAGTCATCAACTGCAAACCTTGGTTCATAGAAG
TGCCATAAAACTCGTCACAATTGAATGTGGGCGCATTCTTGCCACAGGAACCGAGTGA
CCCATGGATCAGTCATCCATGCATTCTGACCATGCACAGACAGTAATTCCATATAATCCT
TCAAGTCATGAGAGTTGGATCAAGTGGTGAAGAAAAAGAGGCAATGAACACCCAGGGAA
AGTGGCAAAGCTTATGCCAAAGCTTAGGTCTCAGGATTTGATTTGCTCCGGGTAATAGGA
AGAGGAAGTTATGCCAAAGACTGTGTTAATGATGATGAGGGATATTGATTGGGACAGACA
ATGAAAGTTGTGAAAAAAGAGCTTGTGTTAATGATGATGAGGGATATTGATTGGGACAGACA
GAGAAGCATGTGTTGAGCAGGCATCCAATCATCCTTCTTGTGTTGGCTGCATTCTGC
TTTCAGACAGAAAGCAGATTGTTCTTGTATAGAGTATGTAATGGAGGAGACCTAATG
TTTCATATGCAGCGACAAAGAAAATTCCTGAAGAACATGCCAGATTTACTCTGCAGAA
ATCAGTCTAGCATTAAATTATCTTCATGAGCGAGGGATAATTATAGAGATTGAAACTG
GACAATGTATTACTGGACTCTGAAGGCCACATTAAACTCACTGACTACGGCATGTGTAAG
GAAGGATTACGGCCAGGGAGATAACACAGCACTTCTGTGGTACTCCTAATTACATTGCT
CCTGAAATTAAAGAGGAGAAGATTGGTTCACTGTTGACTGGTGGCTCTGGAGTG
CTCATGTTGAGATGATGGCAGGAAGGTCTCCATTGATATTGTTGGGAGCTCGATAAC
CCTGACCAGAACACAGAGGATTATCTCTCCAAAGTTATTGGAAAAAACAAATTGCGATA
CCACGTTCTGTCTGTAAGCTGCAAGTGTCTGAAGAGATTCTTAATAAGGACCT
AAGGAACGATTGGGTTGTCATCCTCAAACAGGATTGCTGATATTCAAGGGACACCGTTC
TTCCGAAATGTTGATTGGGATATGATGGAGCAAAACAGGTGGTACCTCCCTTAAACCA
AATATTCTGGGAATTGGTTGGACAATTGATTCTCAGTTACTAATGAACCTGTC
CAGCTCACTCCAGATGACGATGACATTGTGAGGAAGATTGATCAGTCTGAATTGAGGT
TTTGAGTATATCAATCCTTTGATGTCAGAAGAATGTGTCATCCTCATTTTC
AACCATGTATTCTACTCATGTTGCATTTAATGCATGGATAAAACTGCTGCAAGCCTGGA
TACAATTAAACCATTTATATTGCAACCTACAAAAAACACCCAATATCTCTCTTGTA
ACTATATGAATCAATTATTACATCTGTTTACTATGAAAAAAATTAAATACTACTAGCT
TCCAGACAATCATGTCAAAATTAGTTGAACGGTTTCAGTTTAAAGGCCTACAG
ATGAGTAATGAAGTTACCTTTGTTAAAAAAAG

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FIGURE 14

MSHTVAGGGSGDHSHQVRVKAYYRGDIMITHFEPSISFEGLCNEVRDMCSFDNEQLFTMK
WIDEEGDPCTVSSQLELEEAFLRYELNKDSLELIHVPCVPERPGMPCPGEDKSIYRRGA
RRWRKLYCANGHTFQAKRFNRRAHCAICTDRIWGLGRQGYKCINCKLLVHKCHKLVTIE
CGRHSLPQEPMQSSMHSDDHAQTVIPYNPSSHESLDQVGEEKEAMNTRESGKASSSL
GLQDFDLLRIGRGSYAKVLLVRLKKTDRUYAMKVVKELVNDDDEDIDWVQTEKHVFEQA
SNHPFLVGLHSCFQTESRLFFVIEYVNGGDLMFHMQRQRKLPPEHARFYSAEISLALNYL
HERGIIYRDLKLDNVILDSEGHIKLTDYGMCKEGLRPDDTTFCGTPNYIAPEILRGED
YGFSDVWWALGVLFEMMAGRSPFDIVGSSDNPDQNTEDYLFQVILEKQIRIPRSLSVKA
ASVLKSFLNKPDKERILGCHPQTGFADIQGHPFFRNVDWDMMEQKQVVPPFKPNISGEFGL
DNFDSQFTNEPVQLTPDDDDIVRKIDQSEFEGFEYINPLLMSAEECV

N-glycosylation site.

533-536

Tyrosine kinase phosphorylation site.

265-271

N-myristoylation site.

7-12
308-313
394-399

Cell attachment sequence.

24-26

Serine/Threonine protein kinases active-site signature.

365-377

Protein kinase domain
245-513

Protein kinase C terminal domain
514-580

Phorbol esters/diacylglycerol binding domain
132-181

Octicosapeptide repeat
56-85

FIGURE 15

GC GG CG GG CG GG CG CAG TT GCT CATA CTT GTG ACT T GCG GT CAC AGT GG CATT CAG C
TCC AC ACT TGG TAG AACC ACAGG CAC GACA AGC ATAG A A A C AT CCT A A C A T C T C A T C
GAGG C AT CG AGG TCC AT C C C A A T A A A A C T CAG GAG A C C T G G C T A T C A T A G A C C T T A G T C
TTC G C T G G T A T A C T C G C T G C T G C A A C C A G C G G T G A C T T T T T A A G C C T C T T T T T
C T C T T T A C C A G T T T C T G G A G C A A T T C A G G T T T G C C T C T G G A T T G T A A A T T G T A A T G
A C C T C A A A A C T T T A G C A G T T C T T C A T C T G A C T C A G G T T T G C T C T G G C G G T C T C A G
A A T C A A C A T C C A C A C T C C G T A T T A T C T G C G T G C A T T T G G A C A A A G C T C C A A C C A G G
A T A C G G G A A G A A G A A T T G G C T G G T G A T C T T C A G C A G G T T T C T T C A T G G A G G A A C T T A A T
A C A T A C C G T C A G A A G C A G G G A G T A G T A C T T A A A T A T C A A G A A C T G C T A A T T C A G G A C C T
C C A C A T G A T A G G A G G T T A C A T T C A A G T T A T A T A G A T G G A A G A G A A T T C C A G A A G G T
G A A G G T A G A T C A A A G A A G G A A G C A A A A A T G C C G C A G C C A A T T A G C T G T G A G A T A C T T
A A T A A G G A A A A G A A G G C A G T T A G T C C T T A T T A T G A C A C A A C G A A T T C T C A G A A G G A
T T A T C C A T G G G G A A T T A C A T A G G C C T T A T C A A T A G A A T T G C C C A G A A G G A A A G A C T A A C T
G T A A A T T A T G A A C A G T G T G C A T C G G G G T G C A T G G G C C A G A A G G A T T T C A T T A A A T G C
A A A A T G G G A C A G A A A G A A T A T A G T A T T G G T A C A G G T T C A T C A A A C A G G A A C C A A A C A A
T T G G C G C T A A T T C C A T A T C T C A G A T A T T C A G A A G A A A A C C T C A G T G A A A A T C T G A C
T A C C T G T C C T C T G G T T C T T G C T A C T A C G T G T G A G T C C C A A A G C A A C T C T T A G T G A C C
A G C A C A C T C G C T T C T G A A T C A T C T G A A G G T G A C T T C T C A G C A G A T A C A T C A G A G A T A
A A T T C T A A C A G T G A C A G T T A A A C A G T T C T T C G T G C T T A T G A A T G G T C T C A G A A A T A A T
C A A A G G A A G G C A A A A A G A T C T T G G C A C C C A G A T T T G A C C T C C T G A C A T G A A A G G A A C A
A A G T A T A C T G G A C A A G A G G T T G G C A T G G A T T T A A A G G A A A T A G A A T T A A T T G G C T C A
G G T G G A T T T G G C C A A G T T T C A A A G C A A A A C A C A G A A T T G A C G G G A A A G A C T T A C G T T A T T
A A A C G T G T T A A A T A A T A A C G A G A A G G C G G A G C G T G A A G T A A A A G C A T T G G C A A A A C T T
G A T C A T G T A A A T A T G G T C A C T A C A T G G C T G T G G G A T G G A T T T G A T T A T G A T C C T G A G
A C C A G T G A T T C T G A G A G C A G T G A T T A T G A C T C G C T G A G A A C A G C A A A A A T A G T T C A
A G G T C A A A G A A G A C A G A T G C C T T C A T C C A A A T G G A A T T C T G T G A T A A A G G G A C C T T G G A
C A A T G G A T T G A A A A A G A A G G G C G A G A A A C T A G A C A A A G T T T G G C T T T G G A A C T C T T
G A A C A A A T A A C A A A A A G G G G T G G A T T A T A T A C A T T C A A A A A T T A A T T C A T A G A G A T C T T
A A G C C A A G T A A T A T A T T C T T A G A T A C A A A C A A G T A A A G A T T G G G A G C T T G G A C T T
G T A A C A T C T G A A A A A T G A T G G A A A G C G A A C A A G G G A G T A A G G G A A C T T T G C G A T A C A T G
A G C C C A G A A C A G A T T T C T C G C A A G A C T A T G G A A A G G A A G T G G A C C T C T A C G C T T T G G G
C T A A T T C T G C T G A A C T C T T C A T G T A T G T G A C A C T G C T T T G A A A C A T C A A A G T T T C
A C A G A C C T A C G G G A T G G C A T C A T C T C A G A T A T T T G A T A A A A A G A A A A A C T C T T C
C A G A A A T T A C T C T C A A A G G A A C C T G A G G G A T C G A C C T A A C A C A T C T G A A A A T C A A G G A C C
T T G A C T G T G G A A G G A A A A G C C C A G G G A G A A A A A G C A C A C A C A T G T T A G A G C C C T T C
G A A A A A G T A T C T G C T T C T G A T A T G C A G T T T C C T T A A A T T C T A A A A T C T G C T A G G G A
A T A T C A A T G A T A T T A C C T T T A T T T A A T G T T C C T T A A A T T T T A C T A T T T T A C T
A A T C T T T C T G C A G A A A C A G A A A G G G T T T C T T C T T T G C T C A A A A A C A T T C T T A C A T T
T A C T T T T C T G G C T C A T C T C T T A T T C T T T T T T T A A A G A C A G A G G T C T G C T C
T G T T G C C C A G G C T G G A G T G C A A T G A C A C A G T C T T G G C T C A C T G C A A C T T C T G C C T T G G
G T T C A A G T G A T T C T C T G C C T C A G C C T C C T G A G T A G C T G G A T T A C A G G C A T G T G C C A C C
A C C C A A C T A A T T T T G T G T T T T A A T A A A G A C A G G G T T C A C C A T G T G G C C A G G C T G G T
C T C A A A C T C C T G A C C T C A A G T A A T C C A C C T G C C T C G G C T C C C A A G T G C T G G G A T T A C A
G G G A T G A G C C A C C G G C C C A G C C T C A T C T C T G G T T C T A A A G A T G G A A A A A C C A C C C C C A
A A T T T C T T T T A A T A C T A T T A A T G A A T C A A T C A A T C A T C T A T T C A T T T A A T T C T A C
C G C T T T T A G G C C A A A A A A A A T G T A A G A T G C T T C T G C C T C A C A T A G C T T A C A A G G C A G C T
G G A G A A A T A T G G T A C T C A T T A A A A A A A A A A A A A G T G A T G T A C A A C C

FIGURE 16

MAGDLSAGFFMEEILNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREFPEGEGRSK
KEAKNAAAKLAVEILNKEKKAVSPLLLTTTNSSEGLSMGNYIGLINRIAQKRLTVNYEQ
CASGVHGPEGFHYKCKMGQKEYSIGTGSTKQEAQOLAALAYLQILSEETSVKSDYLSSG
SFATTCESQSNSLVTSTLASSESSSEGDFSAUTSEINSNSDSLNSSSLMNGLRNNQRKAK
RSLAPRFDLPDMKETKYTVDKRGMDFKEIELIGSGGFQVFKAKHRIDGKTYVIKRVKY
NNEKAEREVKALAKLDHVNVHYNGCWDGFDYDPETSSDLESSDYDPENSKNSSRSKTK
CLFIQMEFCDKGTLEQWIEKRRGEKLDKVLALELFEQITKGVDYIHSKKLIHRDLKPSNI
FLVDTKQVKIGDFGLVTSKNDGKRTRSKGTLRYMSPEQISSQDYGKEVDLYALGLILAE
LLHVCCTAFETSKFTDLRDGIISDIFDKKEKTLLQKLLSKKPEDRPNTSEILRTLTVWK
KSPEKNERHTC

N-glycosylation site.

91-94
223-226
353-356
528-531

cAMP- and cGMP-dependent protein kinase phosphorylation site.

39-42
112-115

Tyrosine kinase phosphorylation site.

285-293

N-myristoylation site.

95-100
99-104
145-150
180-185
231-236
325-330
434-439
475-480

Amidation site.

442-445

Serine/Threonine protein kinases active-site signature.

410-422

Protein kinase domain
267-538

Double-stranded RNA binding motif

10-75
101-165

FIGURE 17

ATGTCTCGGGAGTCGGATGTTGAGGCTCAGCAGTCTCATGGCAGCAGTGCCTGTTCACAG
CCCCATGGCAGCGTTACCCAGTCCAAGGCTCCTCCTCACAGTCCAGGGCATATCCAGC
TCCTCTACCAAGCACGATGCCAAACTCCAGCAGTCCTCCTCACACTCAGCTCTGGGACACTG
AGCTCCTTAGAGACAGTGTCCACTCAGGAACACTTCTATTCTATTCCCTGAGGACCAAGAACCT
GAGGACCAAGAACCTGAGGAGCCTACCCCTGCCCCCTGGGCTCGATTATGGGCCCTTCAG
GATGGATTGCCAATCTTGAATGTGTGAATGACAACACTGGTTGGGAGGGACAAAAGC
TGTGAATATTGCTTGATGAACCACTGCTGAAAAGAACAGATAAAATACCGAACATACAGC
AAGAAAACACTTCCGGATTTTCAAGGAAAGTGGGTCTAAAAACTCTTACATTGCATACATA
GAAGATCACAGTGGCAATGGAACCTTGTAAATACAGAGCTGTAGGGAAAGGAAACGC
CGTCCTTGAATAACAATTCTGAAATTGCACTGTCACTAACAGAAAATAAGTTTGTCT
TTTTTGATCTGACTGTAGATGATCAGTCAGTTATCTAAGGCATTAAGAGATGAATAC
ATCATGTCAAAAACCTTGGAAAGTGGTGCCTGTGGAGAGTAAAGCTGGCTTCGAGAGG
AAAACATGTAAGAAAGTAGGCCATAAAAGATCATCAGCAAAAGGAAGTTGCTATTGGTTCA
GCAAGAGAGGGCAGACCCAGCTCAATGTTGAAACAGAAAATAGAAATTGAAAGCTA
AATCATCCTGATCATCAAGATTAAAAACTTTTGATGTCAGAAGATTATTATATTGTT
TTGGAATTGATGGAAGGGGGAGAGCTGTTGACAAAGTGGTGGGAATAACCGCCTGAAA
GAAGCTACCTGCAAGCTCTATTACCACTGACTTAAAGCCAGAGAATGTTTACTGTCATCTCAAGAAGAG
GACTGTCCTATAAAGATTACTGATTGGGACTCCAAGATTGGGAGAGACCTCTC
ATGAGAACCTTATGGAACCCCCACCTACTTGGCCTGAAGTTCTGTTCTGTTGGG
ACTGCTGGGTATAACCGTGTGGACTGCTGGAGTTAGGAGTTATTCTTTATCTGC
CTTAGTGGGTATCCACCTTCTGTGAGCATAGGACTCAAGTGTCACTGAAGGATCAGATC
ACCAGTGGAAAATACAACCTCATTCTGAAGGTCTGGGAGAAGTCTCAGAGAAAGCTCTG
GACCTTGTCAAGAAGTTGGTAGTGGATCCAAGGCACGTTTACGACAGAAGAACCC
TTAAGACACCCGTGGCTCAGGATGAAGACATGAAGAGAAAGTTCAAGATCTCTGTCT
GAGGAAAATGAATCCACAGCTCTACCCAGGTTCTAGGCCAGCCTCTACTAGTCGAAAG
CGGCCCGTGAAGGGGAAGCCGAGGGTGCCGAGACCACAAAGCGCCAGCTGTGTGCT
GCTGTGTTGAACTCCGTGGTTGAACACGAAAGAAATGTCCTTTCACTCTGCATC
TTCTTTCTTGAGTCGTTTATAGTTGGATTTAATTATGGAATAATGGTT

FIGURE 18

MSRESDVEAQSHGSSACSQPHGSVTQSQGSSSQSGISSLSTSTMPNSSQSSHSSGTL
SSLETVSTQELYSIPEDEQEPEDQEPPEPTPAPWARLWALQDGFAVNDNYWFGRDKS
CEYCFDEPLLKRTDKYRTYSKKHFRREVGPKNSYIAYIEDHSGNGTFVNTELVGKGKR
RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALREYIMSKTLGSGACGEVKLAFER
KTCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKLNHPCIIKIKNFFDAEDYYIV
LELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSQEE
DCLIKITDFGHSKILGETSLMRTLCGPTYLAPEVLVSGTAGYNRAVDCWSLGVILEFIC
LSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKKLLVDPKARFTTEEA
LRHPWLQDEDMRKRFQDLLSEENESTALPQVLAQPSTSRRKPREGEAEGAETTKRPAVCA
AVL

N-glycosylation site.

48-51
166-169
185-188
503-506

Glycosaminoglycan attachment site.

164-167

Tyrosine kinase phosphorylation site.

289-297

N-myristoylation site.

14-19
37-42
58-63
167-172
227-232
529-534

Amidation site.

177-180

Serine/Threonine protein kinases active-site signature.

343-355

Protein kinase domain

220-486

FHA domain

113-192

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FIGURE 19

GGCACGAGTAGGGGTGGCGGGTCAGTGCTGCTCGGGGGCTTCTCCATCCAGGTCCCTGGA
GTTCTGGCCCTGGAGCTCCGCACTGGCGCGAACCTGCGTGAGGCAGCGCAGCTCTG
GCGACTGGCGGGCATGCCCTCCGGCTGAGGACTATGAAGTGTGTACACCATTGCGA
CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGAGATTAGTT
GGAAAGAACCTGACTATGGCTCCATGACAGAAGCTGAGAAACAGATGCTTGTGTTCTGAAG
TGAATTGCTCGTGAECTGAAACATCCAAACATCGTCTGTTACTATGATCGGATTATG
ACCGGACCAATAACACACTGTACATTGAAATTGTGAAGGGAGGGATCTGGCTA
GTGTAATTACAAAGGGAAACCAAGGAAAGGCAATACTTAGATGAAGAGTTGTTCTCGAG
TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGCGAAGTGTGTTGGTCATA
CCGTATTGCATCGGGATCTAAACCAGCCAATGTTCTGGATGGCAAGCAAAACGTCA
AGCTTGGAGACTTGGCTAGCTAGAATATAACCATGACACGAGTTTGCACAAACAT
TTGTTGGCACACCTTATTACATGTCCTGAACAAATGAATCGCATGTCCTACAATGAGA
AATCAGATATCTGGTATTGGGCTGCTGCTGTATGAGTTATGTCATTAATGCTCCAT
TTACAGCTTTAGCCAGAAAGAACCTGCTGGGAAATCAGAGAAGGCAAATTCAGGCGAA
TTCCATACCGTTACTCTGATGAATTGAATGAAATTATACGAGGATGTTAAACTTAAAGG
ATTACCATCGACCTCTGTTGAAGAAATTCTGAGAACCCCTTAATAGCAGATTGGTG
CAGACGAGCAAAGAAGAAATCTGAGAGAAAGAGGGCGACAATTAGGAGAGCCAGAAAAT
CGCAGGATTCAGCCCTGTATTGAGTGAGCTGAAACTGAAGGAAATTCAAGTACAGGAGC
GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTG
TTCGTGAGAGACTAGCAGAGGACAAACTGGTAGAGCAGAAAATCTGTTGAAGAACTACA
GCTTGCTAAAGGAACGGAAGTTCTGTCCTGGCAAGTAATCCAGAACTTCTTAATCTC
CATCCTCAGTAATTAAAGAACGAAAGTTCAATTCTCAGTGGGAAAGTAAAGAGAACATCATGA
GGAGTGAGAATTCTGAGAGCTCAGCTCACATCTAAGTCCAAGTGCAAGGACCTGAAGAAA
GGCTTCACGCTGCCAGCTGCGGGCTCAAGCCCTGTCAGATATTGAGAAAATTACCAAC
TGAAGCAGACAGATCCTGGGCATGGC~~T~~ACCCAGGTAGAGAGACACAGAGCTGTGAC
AGGATGTAATTACCAACCTTAAAGACTGATATTCAAATGCTGTAGTGTGAATACTT
GGCCCCATGAGCCATGCCCTTCTGTATAGTACACATGATATTTCGGAATTGGTTTACTG
TTCTCAGCAACTATTGTACAAATGTCACATTAAATTTCCTTCTTTAAGAAC
ATATTATAAAAAGAATACTTCTGGTTGGCTTTAATCCTGTTGTGATTACTAGTAG
GAACATGAGATGTGACATTCTAAATCTGGAGAAAAAATAATTAGGAAAAAAATT
TATGCAGGAAGAGTAGCACTCACTGAATAGTTAAATGACTGAGTGGTATGCTTACAAT
TGTCACTGCTAGATTAAATTAAAGTCTGAGATTAAATGTTTGAGCTTAGAAAC
CCAGTTAGATGCAATTGGTCATTAATACCATGACATCTGCTTATAAAATTCCATTGC
TCTGTAGTTCAAACTGTTAGCTTGTGAAAATTCACTGACTGTGATGTTGTATTCTTT
TTTTCTGTTAACAGAATATGAGCTGTCATTTACCTACTTCTTCCACTAA
TAAAAGAATTCTCAGTTA

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FIGURE 20

MPSRAEDYEVLYTIGTGSYGRQCQKIRRKSDGKILVWKELDYGSMTEAEKQMLVSEVNLLR
ELKHPNIVRYYDRIIDRTNTTLYIVMEYCEGGDLASVITKGTKEROYLDEEFVLRVMTQL
TLALKECHRRSDGGHTVLRDLK PANVFLDGKQNVKLGDFGLARILNHDTSFAKTFVGT
YYMSPEQMNRMSYNEKSDIWSLGCILLYELCALMPPFTAQSQKELAGKIREGKFRRIPYRY
SDELNEIIITRMLNLKDYHRPSVEEILLENPLIADLVADEQRRNLERRGRQLGEPEKSQDSS
PVLSELKLKEIQLQERERALKAREERLEQKEQELCVRERLAEDKLARAENLLKNYSLLKE
RKFLSLASNPELLNLPSVIKKVHFSGESKENIMRSENSESQLTSKSKCKDLKKRLHAA
QLRAQALSDIEKNYQLKSRQILGMR

N-glycosylation site.

79-82
354-357

cAMP- and cGMP-dependent protein kinase phosphorylation site.

26-29

Tyrosine kinase phosphorylation site.

100-107

N-myristoylation site.

91-96

Leucine zipper pattern.

306-327
313-334

Serine/Threonine protein kinases active-site signature.

137-149

Protein kinase domain
8-271

FIGURE 21

TTGGCGGGCGGAAGCGGCCACAAACCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA
GCCGCGTCTCTCAGGACAGCAGGCCCTGTCCTCTGCGGGCGCGCTCAGCCGTGCC
TCCGCCCTCAGGTTCTTTCTAATTCCAATAAACTTCAAGAGGACTATGAAAGATT
ATGATGAACTTCTCAAATATTATGAATTACATGAAACTATTGGGACAGGTGGCTTGCAA
AGGTCAAACCTGCCTGCCATATCCTACTGGAGAGATGGTAGCTATAAAATCATGGATA
AAAACACACTAGGGAGTGATTGCCCGGATCAAACGGAGATTGAGGCCTGAAGAAC
TGAGACATCAGCATATATGTCAACTTACCATGTGCTAGAGACAGCCAACAAAATATCA
TGGTTCTTGAGTACTGCCCTGGAGGGAGAGCTGTTGACTATATAATTCCAGGATGCC
TGTCAAGAGGGAGACCCGGGTTGTCTTCCGTCAAGATAGTATCTGCTGTTGCTTATGTC
ACAGCCAGGGCTATGTCACAGGGACCTCAAGCCAGAAAATTGCTGTTGATGAATATC
ATAAATTAAAGCTGATTGACTTTGGTCTGTGCAAACCCAAGGGTAACAAGGATTACC
ATCTACAGACATGCTGTGGAGTCTGGCTTATGCAACGCACTGAGTTAATAACAGGCAAAT
CATATCTGGATCAGAGGAGCATGGGAGATGTTGGAGCATGGCATACTGTTATATGTTCTTATGT
GTGGATTCTACCATTTGATGATAATGTAATGGCTTATACAAGAAGATTATGAGAG
GAAAATATGATGTTCCAAGTGGCTCTCCTCCAGTAGCATTCTGCTTCTTCAACAAATGC
TGCAGGGGACCCAAAGAAACGGATTCTATGAAAATCTATTGAACCATCCTGGATCA
TGCAAGATTACAACATACCTGTTGAGTGGCAAAGCAAGAATCCTTTATTACACCTCGATG
ATGATTGCGTAACAGAACTTTCTGTACATCACAGAAACACAGGAAACAAATGGAGGATT
TAATTTCACGTGGCAGTATGATCACCTCACGGCTACCTATCTCTGCTTCTAGCCAAGA
AGGCTGGGAAAACCAGTCGTTAAGGCTTCTTCTCCTGTGGACAAGCCAGTG
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG
ATAAAAATTATGTGGGGGATTAATAGACTATGATTGGTGTGAAGATGATTATCAACAG
GTGCTGCTACTCCCGAACATCACAGTTACCAAGACTGGACAGAATCAAATGGGGTGG
AATCTAAATCATTAACCTCCAGCCTTATGCAAGACACCTGCAAATAAAATTAAAGAACAAAG
AAATGTATATACTCTTAAGTCTGCTGTAAGAAGACTTCTTATGTTCTGAGC
CAAAGACTCCAGTTAATAAGAACAGCATAAGAGAGAAACTACTACGCAAATCGTT
ACACTACACCCCTCAAAGCTAGAAACCACTGCGCTGAAAGAAACTCCAATTAAACCCAG
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTCTATTAGCCTGAGAGGGCGGTGCC
GCTCAGTGGATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG
CCAAAGTGGTGGAGCCTGAAAGGGGTTGGATAAGGTATCTACTGTGCTCACAGGA
GCAAAGGAAGGGTCTGCCAGAGACGGGCCAGAAGACTAAAGCTCACTATAATGTGA
CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTCAA
AGAAGCATGTTGACTTTGACAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT
TTGGGAAAGTGACAATGCAATTGAATTAGAAGTGTGCCAGCTTCAAAACCGATGTGG
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCCTGGGTTACAAAAGATAGTGGAAAG
ACATCCTATCTAGCTGCAAGGTATAATTGATGGATTCTTCCATCCTGCCGGATGAGTGTG
GGTGTGATACAGCCTACATAAGACTGTTATGATCGCTTGATTAAAGTTCAATTGGAA
CTACCAACTTGTCTAAAGAGCTATCTTAAGACCAATATCTCTTGTGTTAAACAAA
GATATTATTTGTGATGAATCTAAATCAAGCCCCTGTCATTGTTACTGTCTTTT
TAATCATGTGGTTTGATATTAATAATTGTTGACTTCTTAGATTCACTCCATATGTG
AATGTAAGCTCTTAACATATGTCTTTGTAATGTGAAATTCTTCTGAAATAAAACCAT
TTGTGAATAT

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FIGURE 22

MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSIDLPIKTEIEA
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV
AYVHSQGYAHRLDKPENLLFDEYHKLKLIDFGLCAKPKGNKDYHLQTCCGSLAYAAPELI
QGKSYLGSEADVWSMGILLYVLMCGFLPFDNVMALYKKIMRGKYDVPKWLSPSSILL
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFIHLDDDCVTELSVHHRNNRQT
MEDLISLWQYDHLTATYLLLAKKARGKPVRLSFSFGQASATPFTDIKSNNWSLEDV
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESGVESKSLTPALCRTPANKL
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI
KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHMEETPKRKGAKVFGSLERGLDKVITV
LTRSKRKGSARDGPRRLKLHYNVTTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQT
QSDFGKVTMQFELEVQCLQKPDVGIRRQLKGDAWVYKRLVEDILSSCKV

N-glycosylation site.

354-357
485-488
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253
546-549

Tyrosine kinase phosphorylation site.

2-10
421-427
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain
11-263

Kinase associated domain 1
602-651

FIGURE 23

GTCTTTATTCAGTCCCGGATCCGGGGCGCAGGCCAGCTCAGGCCCCAGGGATGGAC
GTCGTGGACCCCTGACATTTCATAAGAGACCCCCGGGACACTATGACCTGCTACAGCGG
CTGGGTGGCGGACGTATGGGAAGTCTTAAGGCTCGAGACAAGGTGTCAAGGGACCTG
GTGGCACTGAAGATGGTAAGATGGAGCTGATGATGATGTCCTCACCATGGAGTTATCTC
ATCCTCATATTGAAAACCTGCCGGACGCCAACATCGTGGCCTACCATGGAGTTATCTC
TGGTTGCAGAAACTCTGGATCTGCATGGAATTCTGTGGGCTGGTCTCTCAGGACATC
TACCAAGTACAGGCTCCCTGTCAGAGCTCCAGATTAGCTATGTCAGGCCAGTGC
CAGGGACTGGCCTATTGCACTCACAGAAGAAGATAACACAGGGACATCAAGGGAGCTAAC
ATCCTCATCAATGATGCTGGGAGGTCAGATTGGCTGACTTTGGCATCTGGCCCAGATT
GGGGCTACACTGCCAGACGCCCTCTCTTCAATTGGACACCCCTACTGGATGGCTCCGAA
GTGGCAGCTGTGGCCCTGAAGGGAGGATAACAATGAGCTGTGACATCTGGTCCCTGGC
ATCACGGCCATCGAACCTGGCGAGCTACAGCCACCGCTTTGATGTCACCCCTCAGA
GTTCTCTTCCATGACCAAGAGTGGCTACCAGCCTCCCCACTGAAGGAAAAAGGCAA
TGGTCGGCTGCCTTCCACAACCTCATCAAAGTCACTCTGACTAAAGGTCCCAGAAACGA
CCCAGCGCCACCAAGATGTCAGTCATCAACTGGTATCCCAGCCTGGCTGAATCGAGGC
CTGATCCTGGATCTTCAACTGAAGAAATCCCAGGAAAGGACCCCTCCATTGGGAC
ATTGAGGATGAGGAGCCCAGCTACCCCTGCTATCCCTCGCGGATCAGATCCACCCAC
CGCTCCAGCTCTGGGGATCCCAGATGCAAGACTGCTGTCGGCGCACATGGAGTTCA
AAGCTCGAGGAATGGAGACCAGACCCCCAGCCAACACCGCTGCCCTACAGCCTCTGA
GACCTCAGGAGCAGCAGCCCCAGGAAGCAACTGTCAGAGTGTGACGATGACTATGAC
GACGTGGACATCCCCACCCCTGCAAGAGGACACACCTCCTCCACTCCCCCAAGCCCAAG
TTCCGTTCTCCATCAGACGAGGGCTGGGAGCATGGGGATGATGGGCAGCTGAGCCG
GGGGTCTGGTCCGGTGTGCCAGTGGGCCCCACCAAACAGCCCCGTCCTGGGCTCTCC
CCATCCACCAGCAGCCCCACCTCACCGCCATTCAAGAACCCCTACTCTGGAACCCACCC
TCCCAGGAGCTTGACAAGCCCCACTTCTGCCCCCAAGAAGGAAAAGATGAAGAGAAAG
GGATGTGCCCTCTCGTAAAGTTCAATGGCTGCCCTCGGATCCACAGCACGGCC
GCCTGGACACATCCCTCACCAAGGACCGACCTGCTCTGGGGCAGAGGAAGGCATC
TTCATCCTGAACCGGAATGACCAAGGAGCCACGCTGGAAATGCTCTTCTAGCCGGACT
ACGTGGGTGACTCCATCAACACGTTCTCATGTCCTCTCAGGAAAGACCCCCCACCTG
TATTCTCATAGCATCCTGGCTGCTGGAACGGAAAGAGACAGAGCAGGAAACCCCCATC
GCTCACATTAGCCCCACCGCTACTGGCAAGGAAGAACATGGTTCCACCAAGATCCAG
GACACCAAGGCTGGGGCGTGTGTGGCGAGGGTGCAGCTCTGGGGCCGTC
CTGTGGGGCATTGGAGACGTCGGTGTCTGCTCTGCTTCACTGGTACCGCCATGAACAAA
TTCTGCTTGTCCGGAGGTGCTGTTCCACTGCGACGCCCTCTGCGTGTGCGCTG
CTGACCGGGCCAGGCTCTGAGCTGCCGCTGTGTCATCGCGTGA
GGGAAGTCGGTGTCTCCACACGGTGCCTTGGCGCGCTCTGCTGGCTGGCGAG
ATGAGCACCGAGCACAGGGACCCGTGCAGGTGACCCAGGTAGAGGAAGATATGGTATG
GTGTTGATGGATGGCTCTGTGAAGCTGGTGACCCGGAGGGTCCCCAGTCGGGGACTT
CGCACACCTGAGATCCCCATGACCGAAGCGGTGGAGGGCGTGGCTATGGTTGGAGGTCA
CTTCAGGCCCTCTGGAAGACATGGAGTGCAGGTGTGGCTCTAGGCTGGATCAGCTGCTA
CAGGAGCTGAGAGACCCCTACCCCTACTTCCGTCTGCTTGGCTCCCCCAGGCTGGAGTGC
AGTGGCACGATCTGCCACTGCAACCTCCCTCCAGGTTCAAGCAATTCTCCTGCC
TCAGCCTCCCGAGTAGGGATTACAGGCCGTGAGTGGTGGAGACACGCCAGTGGATG
ATCCTACTGCTCCAGCAACCTCTACATCCAGGAATGAGTCCCTAGGGGGGTGTCAAGGAA
CTAGTCCTGCACCCCTCCCCATAGACACACTAGTGGTCAATGGCATGTCCTCATCTCC
CAATAAACATGACTTTAGCCTCTGCAAAAAAA

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FIGURE 24

MDVVDPDIFNRDPRDHYDLLQRLGGGTYGEVFKARDKVGDLVALKMVKMEPDDDVSTLQ
 KEILILKTCRHANIVAYHGSYWLQKLWICMEFCGAGSLQDIYQVTGSLSELOQISYVCRE
 VLOGLAYLHSQKKIHRDIKGANILINDAGEVRLADFGISAQIGATLARRLSFIGTPYWMA
 PEVAAVALKGGYNELCDIWSLGITAIELAELQPPLFDVHPLRVLFLMTKSGYQPPRLKEK
 GKWSAAFHNFIKVTLTKSPKKRPSATKMLSHQLVSQPGLNRLGILLDLKDKNPGKGPSI
 GDIEDEEPELPPAIPRRIRSTHRSSSLGIPDADCCRHHMEFRKLRGMETRPPANTARLQP
 PRDLRSSSPRKQLESESSDDDYDDVDIPTPAEDTPPPPLPPKPKFRSPSDEGGPSMGDDGQL
 SPGVLVRCASGPPPNSPRPGPPPSTSSPHLTAHSEPSLWNPPSRELDKPPPLPPKKEKMK
 RKGCALLVLFNGCPLRIHSTAATHPSTKDQHLLLGAEEGIFILNRNDQEATLEMLFPS
 RTTWVYSINNVLMSLSGKTPHLYSHSILGLLERKETRAGNPIAHISPHRLLARKNMVSTK
 IQDTKGCRACCVVAEGASSGGPFLCGALETSVVLLQWYQPMNKFLVRQVLFPLPTPLSVF
 ALLTGPSELPAVCIGVSPGRPGKSVLFHTVRFGALSCWLGEMSTEHRGPVQVTQVEEDM
 VMVLMGDSVKLVTPEGSPVRLRTPEIPMTEAVEAVAMVGGQLQAFWKHGVQVWALGSDQ
 LLQELRDPTLTFRLLGSPRLECSGTISPHCNLLPGSSNSPASASRVAGITGL

CAMP- and cGMP-dependent protein kinase phosphorylation site.

168-171
 261-264
 573-576

N-myristylation site.

25-30
 163-168
 278-283
 328-333
 517-522
 579-584
 606-611
 615-620
 625-630
 676-681
 694-699
 761-766

CNH domain
 500-805

Protein kinase domain

17-274

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FIGURE 25

GAATTGGCACGAAGGAGAGTAGCAGTGCCTGGACCCAGCTCCTCCCCTTCTCT
CTAAGGATGGCCAGAAGGAGAACTCCTACCCCTGGCCCTACGCCGACAGACGGCTCCA
TCTGGCCTGAGCACCTGCCAGCGAGCTCCGGAAAGAGCCTGTACCCATCTGCA
CTTGTCCCTCATGAGCCGCTCCAATGTCAGGCCACAGCTGCCCTGGCCAGAAGGTGATG
GAGAATAGCAGTGGGACACCCGACATCTAACGCGGCACTTCACAATTGATGACTTGAG
ATTGGGCGCTCTGGGAAAGGCAAGTTGGAAACGTGTACTGGCTCGGGAGAAGAAA
AGCCATTTCATCGTGGCCTCAAGTCCTTCAAGTCCCAGATAGAGAAGGAGGGCGTG
GAGCATCAGCTGCGCAGAGAGATCGAAATCCAGGCCACCTGCACCATCCAAACATCCTG
CGTCTCTACAACATTTTATGACCGGAGGAGGATCTTGATTCTAGAGTATGCC
CGCGGGGAGCTCTACAAGGAGCTGCAGAAGAGCTGCACATTGACGAGCAGCGAACAGCC
ACGATCATGGAGGAGTTGGCAGATGCTCTAATGTACTGCCATGGAAAGAAGGTGATTCA
AGAGACATAAAGCCAGAAATCTGCTTCTAGGGCTCAAGGGAGAGCTGAAGATTGCTGAC
TTCGGCTGGTCTGTCATGCGACCTCCCTGAGGAGGAAGACAATGTGTGGCACCCCTGGAC
TACCTGCCCTCAGAGATGATTGAGGGCGCATCGACAATGAGAAGGTGGATCTGTGGTGC
ATTGGAGTGCTTGCATGAGCTGCTGGTGGGAACCCATTGAGAGTGCATCACACAAAC
GAGACCTATCGCCGCATCGTCAAGGTGGACCTAAAGTTCCCGCTCTGTGCCAACGGGA
GCCCAAGGACCTCATCTCAAACACTGCTCAGGCATAACCCCTCGGAACGGCTGCCCTGGCC
CAGGTCTCAGCCCACCCCTGGTCCGGGCCAACTCTCGGAGGGTGCCTGCCCTCTGCC
CTTCAATCTGTCGCCTGATGGTCCGTCACTCGGGTGCCTGTGTTGTATGTCTG
TGTATGTATAGGGAAAGAAGGGATCC

FIGURE 26

MAQKENSYPWPYGRQTAPSGLSTLPQRVLRKEPVTPSALVLMRSRSNVQPTAAPGQKV
MENSSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGV
EHLQLRREIEIQAHLLHHPNILRLYNYFYDRRIYIYLLEYAPRGELYKELOQK
SCTFDEQRTATIMEELADALMYCHGKKVIHRDIKPENLLLGLKGE
LKIADFGWSVHATSLRRKTMCGTLDYLPPEMIEGRIDNEKVDLWCIGVLCYELLV
GNPFESASHNETYRRIVKVDLKFPASVPTGAQDLISKLLRHNP
SERLPLAQVSAHPWVRANSRRVLPPSALQSVA

N-glycosylation site.

60-63
278-281

cAMP- and cGMP-dependent protein kinase phosphorylation site.

229-232

Amidation site.

192-195

Serine/Threonine protein kinases active-site signature.

196-208

Protein kinase domain

77-326

FIGURE 27A

GGAATTCCTTTTTTTTTTGAGATGGAGTTCACTCTGGCCAGGCTGGAGTG
 CAATGGCACAATCTCAGCTACTGCAACCTCCGCCTCCCGGTTCAAGCGATTCTCCTGC
 CTCAGCCTCTCAAGTAGCTGGGATTACAGGCATGTGCCACCACCCCTGGCTAACTAATT
 CTTTCTATTTAGAGATGGGTTTACCATGTTGGCTAGGCTGGTCTGAACCTCTG
 ACCTCAGGTGATCCACTTGCCTGGCCTCCAAAGTGCCTAGGATTACAGCGTGAAACTG
 TGCCTGGCTGATTCTTTTGTGTTGGATTTGAAACAGGGTCTCCCTGGTCGCC
 AGGCTGGAGTGCAGTGGTGCATCTGGCTACTATAACCTCACCTCCTGGTTCAAGT
 GATCCTCCCACTTGTGACTGATTACAGGCGTGCACCACACCCGG
 CTAATTTTGTATTTTATTAGAGACAGGGTTTACCATGTTGCCAGGCTGTTCTCAA
 CTCCCTGGACTCAAGGGATCCGCCTGCCTCCACTTCCAAAGTCCGAGATACAGGTGTG
 AGTCACCATGCCTGACCTTATAATTCTTAAGTCATTCTGTTGCTCATTCTCCTAG
 GGTCTCACAAACAAATCTGCATTAGGGTACAATAATCCTTAACCTGATTGATGAA
 AGGAAGATGAAGTATTGATGATTAGAAAGGGAAAGTAGTAAGCCCACGACACTCCT
 GGATGATGATCCTAAATCCAGATACAGTAAAGGGTATGGAAAGGTAGAATACAAAA
 TTGGTTAAATTAAATTATCTAAATATCTAAAACATTGGATACATTGTTGATGTGA
 ATGTAAGACTGTACAGACTTCTAGAAAACAGTTGGGTTCCATCTTCATTCCCCAG
 TGCAGTTCTGAGAAATGGAATCCGAGGATTAAAGTGGCAGAGAATTGACAATTGATT
 CCATAATGAACAAAGTGAGAGACATTAAAATAAGTTAAAATGAAGACCTTACTGATG
 AACTAAGCTGAATAAAATTCTGCTGATACAGATAACTCGGGAACTGTTAACAAA
 TTATGATGATGGCAAAACACCAGAGGACTGGTTGAGTTGCTCAAACAGAGAAAA
 ACAGTGTCCGCTAAGTGATGCTTTAAATAATTGATTGGCTTACAGTCAGCAA
 TGAAAGCGCTTCCCCAGATAAAATGGCCAAAATGAGAGTTGGCTAGAATTCAAGTGA
 GATTGCTGAATTAAAAGCTATTCAAGAGCCAGATGTCACGTGACTACTTCAAATGG
 CCAGAGCAAACGTCAAGAAATTGCTTTGTTCATATATCTTGCACAAATTGAACTGT
 CACAAGGTAATGTCAAAAAAGTAAACAACTTCTCAAAAGCTGTTAGAACAGTGGAGCAG
 TACCACTAGAAATGCTGGAAATTGCCCTGCGGAATTAAACCTCAAAAAAGCAGCTGC
 TTTCAGAGGAGGAAAAGAAGAATTATCAGCATCTACGGTATTAACTGCCAAGAACAT
 TTCCGGTTCACTGGCATTACAGAATAGGAACACAGTTGTGATTCCAGAGGACAGA
 CTACTAAAGCCAGGTTTATATGGAGAGAACATGCCACCACAAAGATGCAGAAATAGGTT
 ACCGGAATTCTTGAGACAAACTAACAAAACATAACAGTCATGCCATTGGAAGAGTCC
 CAGTTAACCTCTAAATAGCCAGATTGTGATGTGAAGACAGATGATTCAAGTTGACCTT
 GTTTATGAAAAGACAAACCTCTAGATCAGAATGCCAGATTGGTTGTGCTGGATCTA
 AACCAAGTGGAAATGATTCTGTAATTAGAAATTAAAGTCTGTTCAAATAGTCATT
 TCAAGGAACCTCTGGTGTAGATGAAAAGAGTTCTGAACATTATTACTGATTCAATAA
 CCTGAGAATAAAACGAATCAAGTCTCTAGCTAAATTAGAAGAAACTAAAGAGTATC
 AAGAACCCAGGGTTCCAGAGAGTAACCAGAAACAGTGGCAAGCTAACAGAAAGTCAGAGT
 GTATTAAACCGAAATCTGCTGCATCTCAAATCACTGGCAGATTCCGGACTAGCCCAGA
 AAGTTAATACAGAGCAGAACATACCACTTTGAGCAACCTGTCTTCAGTTCAAAC
 AGTCACCAACATCTAAATGGTTGACCCAAATCTATTGTAAGACACCAA
 GCAGCAATAACCTTGGATGATTACATGAGCTTTAGAAGACTCCAGTTGTAAGAATGACT
 TTCCACCTGTTGTCAGTTGTCACACCTTATGCCAACCTGCTGTTCCAGCAGCAAC
 AGCATCAAATACTGCCACTCCACTCAAATTTACAGGTTTAGCATCTTCTCAGCAA
 ATGAATGCATTGGTAAAGGAAGAATTATTCCATATTAAAGCAGATAGGAAGTGGAG
 GTTCAAGCAAGGTATTCAGGTGTTAAATGAAAAGAACAGATAATGCTATAAAATATG
 TGAACCTAGAAGAAGCAGATAACCAAACCTCTGATAGTTACCGGAACGAAATAGCTTATT
 TGAATAAACTACAACAAACAGTGATAAGATCATCCGACTTTATGATTGAAATCACGG
 ACCAGTACATCTACATGGTAATGGAGTGTGGAAATTGATCTTAATAGTTGGCTAAAA
 AGAAAAAAATCCATTGATCCATGGGAACGCAAGAGTTACTGGAAAATATGTTAGAGGAG
 TTCAACACAATCCATTGATGTTACAGTGTGATCTTAAACCGAGCTAACCTTCTGA
 TAGTTGATGGAATGCTAAAGCTATTGATTGGGATTGCAAACCAAAATGCAACCGAGATA
 CAACAAGTGTGTTAAAGATTCTCAGGTGGCACAGTTAAATTATGCCACCAGAAC
 TCAAAGATATGTCTCCCTCAGAGAACATGGAAATCTAAGTCAGAACAGATAAGCCCCAAA
 GTGATGTTGGCTTACGGATGTTTGTACTATATGACTTACGGAAAACACCAATTTC
 AGCAGATAATTAAATCAGATTCTAAATTACATGCCATAATTGATCTTAATCATGAAATTG
 AATTCCCGATATTCCAGAGAACAGATCTCAAGATGTGTTAAAGTGTGTTAAAAGGG
 ACCCAAAACAGAGGATATCCATTCTGAGCTCCTGGCTCATCCATTGTTCAAATTCAA
 CTCATCCAGTTAACCAAATGCCAAGGGAACCAACTGAAGAAATGAAATATGTTCTGGGC
 AACCTGTTGGTCTGAATTCTCTAACTCCATTGAAAGCTGCTAAAACCTTATATGAAC
 ACTATAGTGGTGGTGAAGTCATAATTCTCTCATCCTCAAGACTTTGAAAAAAAAGGG
 GAAAAAAATGATTGCAATTGCAATTGTCAGATAGGAGGTATAAAATATATTGGACT
 GTTAACTCTGAATCCCTGTTGAAATCTACATTGAAAGACAACATCACTGAAAGTGT
 ATCAGCAAAAAAAATTCACTGAGATTATCTTAAAGAAAATGTAAGAACACCAC

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FIGURE 27A

TTATGGCACTGTATAATATTGTAGACTTGTCTCTGTTTATGCTCTTGTGTAATCTAC
TTGACATCATTACTCTTGGAAATAGTGGGTGGATAGCAAGTATATTCTAAAAACTTG
TAAATAAAGTTTGTGGCTAAATGA

FIGURE 28

MNKVRDIKNKFKNEDLTDELSNKISADTTDNGTQNQIMMMANNPEDWLSLLLKLEKNS
 VPLSDALLNKLIGRYSQAIIEALPPDKYQGQNESFARIQVRFAELKAIQEPDDARDYFQMAR
 ANCKKFAFVHISFAQFELSQGNVKSKQLLQKAVERGAVPLEMLEIALRNINLQKKQLLS
 EEEKKNLSASTVLTQESFSGSLGHQNRNNSCDSRGQTTKARFLYGENMPPQDAEIGYR
 NSLRQTNKTKQSCPGRVPVNLLNSPDCDVKTDDSVVPCFMKRQTSRSECRDLVPGSKP
 SGNDSCELRNLSVQNSHFKEPLVSDEKSSELIITDSITLKNKTESSLAKLEETKEYQE
 PEVPESNQKQWQAKRKSECINQNPAAASSNHWQIPELARKVNTEQKHTTFEQPVFSVSKQS
 PPISTSKWFDPKSICKTPSSNTLDDYMSCFRTPVVKNDFPACQLSTPYGQ PACFQQQQH
 QILATPLQNLQVLASSSANECISVKGRIYSILKQIGSGGSSKVFQVLNEKKQIYAIKYVN
 LEEADNQTLDSYRNEIAYLNKLQHQHSDKIIRLYDYEITDQYIYVMMECGNIIDLNSWLKKK
 KSIDPWERKSYWKNMLEAVHTIHQHGVHSDLK PANFLIVDGMLKLIDFGIANQMQPDTT
 SVVKDSQVGTVNMPPEAIKDMSSRENGKS SKISPKSDVWSLGCILYYMTYGKTPFQQ
 IINQISKLHAIIDPNHEIEFPDIPEKDLQDVLKCCLKRDPKQRI SIPELLAHPYVQIOTH
 PVNQMAKGTTEEMKYVLGQLVGLNSPNSILKAAKTLYEHYSGGESHNSSSKTFEKKRGK
 K

N-glycosylation site.

90-93
 186-189
 210-213
 247-250
 303-306
 342-345
 546-549
 827-830

cAMP- and cGMP-dependent protein kinase phosphorylation site.

282-285
 374-377
 599-602

Tyrosine kinase phosphorylation site.

351-358
 787-796

N-myristoylation site.

88-93
 297-302
 302-307
 470-475
 516-521
 626-631
 798-803

Amidation site.

838-841

Serine/Threonine protein kinases active-site signature.

627-639

Protein kinase domain

509-775

FIGURE 29

GAATTCCGGGCCGCGTCGACGATCTTGGAGACGGCGACCCAGGCATCTGGGGAGCCAC
 AGAAGTCGTACTCCCTAAACCTGCTTGCTCCCCCTGTGGATGTAACCCCTAGCTGG
 CATTTCGCATCTCAATTGGCTGTGATGGAGGCCTTGGGATTGAGATGGATGAGCC
 AATGGCTTTCTCCCCAGCGTGACCGGTTTCAGGCTGAAGGCCTTAAACAAACGA
 GCAGAATTAAACTTGAGGTGTTAAACAGATATTGAGAAGCTTATGAAGCTGTAC
 ACAGCTTAGTAATGTGTTAAGATTGAGGACAAAATTGAGAAGGCACCTCAGCTGT
 TTATTGCCACAGCACAGTTACAAGTAGGACCTGAAGAGAAAATTGCTCTAAACACTT
 GATTCCAACAAGTCATCCTATAAGAATTGAGCTGAACCTCAGTGCCTAACAGTGGCTGG
 GGGGCAAGATAATGTCATGGAGTTAAATACTGCTTAGGAAGAATGATCATGTAGTTAT
 TGCTATGCCATATCTGGAGCATGAGTCGTTGGACATTCTGAATTCTCTTCCTTCA
 AGAAGTACGGAAATATGCTTAATCTGTTAAAGCTTGAACAGCATTCACTCAGTTGG
 TATTGTTACCGTGATGTTAAAGCCAGCAATTTTATATAATTAGGCCCTGAAAAAGTA
 TGCTTGGTAGACTTGGTTGGCCCAAGGAACCCATGATACGAAAATAGAGCTTCTTAA
 ATTTGTCCAGTCTGAAGCTCAGCAGGAAAGGTGTTACAAAACAAATCCCACATAATCAC
 AGGAAACAAAGATTCCACTGAGTGGCCAGTACCTAACCTAAGGAGCTGGATCAGCAGTCCAC
 AAAAGCTCTGTTAAAGACCCACACAAATGCACAAATTCAGATTAACAAAGGAAAAGA
 CGGAAAGGAGGGATCTGAGGCCCTCTGTCCAGCGCTCTGTTTGAGGAAAGAAAATT
 CAATATACACAGCTCCATTTCACATGAGAGCCCTGAGTAAACTCATGAAGCAGTC
 GACTGTGGATGTACTGCTAGAAAGTTAGCAACAAAAAGAAGGCTATTCTACGAAAGT
 TATGAAATAGTGCTGTGAGGAAAATGCCAGTTGCCCAGCTAGCCTGACCTGTGA
 CTGCTATGCCACAGATAAGTTGAGTTTGCCCTTCAAGGCCCTGAGCAGGTTGCC
 TAGGGCAGGTACACCAAGGATTAGAGCACAGAGGCTTGACAAAGTGGCCCAATCAAAC
 TACAGCAATTGACATGTGGCTGAGGTGTCATATTCTTCTTGCTTAGTGGACGATA
 TCCATTAAAGCAAGTGATGATTAACTGCTTGGCCAAATTATGACAATTAGGGG
 ATCCAGAGAAACTATCCAAGCTGCTAAACATTGGGAAATCAATATTATGAGCAAAGA
 AGTTCCAGCACAAGACTTGAGAAAATCTGTGAGGAGACTCAGGGTATGGATTCTAGCAC
 TCCCAAGTTACAAGTGATATACAAGGGCATGCTCTCATCAACCAGCTATTTCAGAGAA
 GACTGACCATAAAAGCTTCTGCCCTGTTCAAACACCTCCAGGACAATACTCAGGGAAATT
 ATTAAAAAGGGGGATAGTAATAGCTGTGAGCATTGTTGATGAGTATAATACCAATT
 AGAAGGCTGGAATGAGGTACCTGATGAAGCTTATGACCTGCTTGATAAACTCTAGATCT
 AAATCCAGCTTCAAGAATAACAGCAGAAAGCTTGTGACATCCATTAAAGATAT
 GAGCTTGTGATAATTGATCTTAAATGTTACTGTTAGGAGGTTAGAATAAAAGAA
 TACTTTGTAATAGCCACAAGTTGTTAGAGACCAGAGCAGGATTAAATAATTATT
 AACATTAGTGTTGGCAGATTCTAAATATAGATTAAGAATAACTTAAATGCTG
 GGATAGTTCTGGGACTAACACATGATCTTCTTGAGTTAACCTACCTAAGTAGATT
 TAGGTGGGTTCTATTAGGTAGATTAGCTTCTGCTTCAATTACCTTCACTGACATACA
 GAAAAAGGAGCAGTTAGTTAAATTAAACAGATGTGATGAGGATTAAAT
 GAATCAAAGACTTAATTGAGATTCTTCTAGAGTTAGGTTAGGTTAGTTGGGAA
 AACTCAACTGGTGTGGCTCTAACATTGTAATAAGAAGATAATTCTTCTT
 CTAGAGGTACATATTAGGCCCTTATGAAACACTAAACAAATGAGGAAATGTTGGTCATGG
 GGCAAAAGTATCACTTAAATTGAAATTGATCCATTCTTAAACACTTCATGAAAGCATT
 CTGGTGTGAAATTGCCATTCTTCTGCTTCAATTCTTCTCTGCCCCCT
 ACCTAAACATTCTCTCGGAAATTACATGGTGTGACCACAAAGTTCTGGATGTTTA
 TAAATATTGACGTGTTACAGTTGGAAATTAAATACACACTGGTTGATAAAA
 GGGAGCTGCAGGACCAAGGTGAAGATTGATAGTCAAATGCTTCTTGTGAGTTG
 ATATTCTACACCATCTTAGATATAATTAGGTAGTGTGCTGAAAGGAAAAGTGAATACA
 GAATTGACGGTATTATTGGAGATTCTCTGCGTAGAGCCATCCAGATCTGTATCC
 TGTTTGACTAAGTCTTAGGTGGTTGGGAAAGACAGATAATGAAGTAGGCAAAGGAGAAA
 GGACCCAAGGATAGAGGTTATATTGAGAATGGTATATCAATGACAGCATATCAAAC
 TCCTATGGAAAAAGTCTGGTGGTCAGCTGACAGATTCCATTAGTAGTCAG
 AATACAGAAATAGTTAGGGACATGTATTCAATTGTTATTGAGCATTGATAGGT
 CAGTATCTACCTAATCTGTTGGTAAGTATAGGATATAAAACCAATTACCAATTGATCTGTC
 TTATGCCATAATCTTAAAAAAATTGAATGCTTGAATTGATATTCAATAAAAGTTA
 TCCTTTATAAAAAAAAGTCGACGCCCGC

FIGURE 30

MEASLGIQMDEPMAFSPQRDRFQAEGSLKKNEQNFKLAGVKKDIEKLYEAVPQLSNVFKI
EDKIGEGTFSSVYLAQQLQVGPEEKIALKHLIPTSHPIRIAELQCLTVAGGQDNVMGV
KYCFRKNDHVVIAAMPYLEHESFLDILNSLSFQEVREYMLNLFKALKRIHQFGIVHRDVKP
SNFLYNRRLKKYALVDFGLAQGTHDTHKIELLKFKVQSEAQQERCSONKSHITGNKIPLSG
PVPKELDQQSTTKASVKRPTNAQIQIKQGKDGKEGSVGLSVQRSVFGERNFNIHSSISH
ESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASLTCDCYATDKVC
SICLSSRQQVAPRAGTPGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLSGRYPFYKASDD
LTALAQIMTIRGSRETIQAAKTFGKSILCSKEVPAQDLRKLCERLRGMDSTPKLTSQI
GHASHQPAISEKTDHKASCLVQTGGQYSGNSFKKGDSNSCEHCFDEYNTNLEGWNEVPD
EAYDLLDKLLDLNPASRITAEEALLHPFFKDMSL

N-glycosylation site.

226-229
390-393

Tyrosine kinase phosphorylation site.

41-48

N-myristoylation site.

67-72
112-117
119-124
198-203
202-207
432-437
467-472
506-511

ATP/GTP-binding site motif A (P-loop).

439-446

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

58-569

FIGURE 31

CCGAGTTACGAGTCGGC~~AAAGCGGCGGGAAAGTT~~CGTACTGGGCAGAACCGCAGCGACGGGTCT
GCGGCTTAGGTGAAAATGCCTCGTGTAAAGCAGCTCAAGCTGGAAGACAGAGCTCTGCA
AAGAGACATCTTGCAGAACAAATTGCA~~AGTGGAGAGATAATAACTGACATGGCA~~AAAAAG
GAATGGAAAGTAGGATTACCCATTGCCAAGGAGGCTTGGCTGTATATATCTTGTGAT
ATGAATTCTCAGAGTCAGTTGCCAGTGATGCACCTGTGTTGAAAGTGGAACCCAGT
GACAATGGACCTCTTTACTGAATTAAAGTTCTACCAACGAGCTGCAAAACCAGAGCAA
ATT~~TCAGAAATGGATT~~CGTACCCGTAAAGCTGAAGTACCTGGGTGTCCTAAGTATTGGGG
TCTGGTCTACATGACAAAAATGGAAAAAGTTACAGGTTATGATAATGGATCGCTTGGG
AGT~~GACCT~~TCAGAAAATATGAAGC~~AAATGCC~~AAAGGTTTCTGGAAA~~ACTGTCTG~~
CAGCTAACGTTAAGAATTCTGGATATTCTGGAAATATATT~~CACGAGCATGAGTATGTGCA~~
GGAGATATCAAGGCC~~TA~~AAATCTTCTGAACTACAAGAATCTGACCAGGTGACTTG
GTAGATTATGGCCTGCTTATCGGTACTGCCAGAAGGAGTTCAAAAGAAATACAAAGAA
GACCCAAAAGATGT~~CACGATGCC~~ACTATTGAATT~~CACGAGCATG~~ATGCACACAATGGT
GTGGCCCCATCAAGACGTGGT~~GATTGGAA~~ACTTG~~GGTTATTG~~CATGATCCAATGGCTT
ACTGCCATCTCCTGGGAGGATAATTGAAAGATCCTAAATATGTTAGAGATTCCAAA
ATTAGATA~~CAGAGAAA~~ATTGCAAGTTGATGGACAAATGTTCTGAGAAAAACAAA
CCAGGTGAAATTGCCAATACATGGAAACAGT~~GAAATTACTAGACTACACTG~~AAAAACCT
CTTATGAAAATTACGTGACATTCTT~~TGCA~~AGGACTAAAGCTATAGGAAGTAAGGAT
GATGGCAAATTGGACCTCAGTGTGTGGAGAATGGAGGTTGAAAGC~~AAAACA~~ATAACA
AAGAGCGAAAGAAAAGAAATTGAAGAAAGCAAGGAAC~~TGGTGT~~GAAGATA~~CGGA~~ATGG
TC~~AAAACACACAGACAGAGGAGGCC~~ATACAGACCCGTTCAAGAACAGAAAGAGAGTCCAG
AAGTAATTTCAGATGCTG~~TAACCAGATT~~TC~~TTTCTTGT~~TTGACTTTCT
CCTTTCTGTTAGAACTGTTTATT~~TC~~GTGAGTCTGCGAGGTGGAATTAAATGATTA
AAACTCATGTGTTCAAGAAA~~CATAAA~~ACTTTTTATAAAAATATTGTACAATT~~CATT~~
AAAGGCTAATT~~TATGAA~~ATTGAAAATCTCAGGTTA~~ACTCCTAAGT~~TATCCC~~AAAGC~~
CGTGTGTTGTGATGTTGGAGTACATATATGAAAATTATTATGACACGC~~ACTTTC~~
TAATCATTG~~TACATTCTCAGAGTGG~~ATAAAAATGTTGACAAAGTC~~CTC~~ACTTTAAGG
AAATGCAAAGCTTAA~~AAACTCT~~CTCTTTGTTGATG~~CAG~~

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FIGURE 32

MPRVKAAQAGRQSSAKRHLAEQFAVGEIITDMAKKEWKVGLPIQGGFGCIYLADMNSSE
SVGSDAPCVVKVEPSDNGPLFTELKFYQRAAKPEQIOKWIRTRKLKYLGVPKYWGSGLHD
KNGKSYRFMIMDRFGSDLQKIYEANAKRFSRKTVLQLSLRILDILEYIHEHEYVHGDIKA
SNLLNYKNPDQVYLVVDYGLAYRYCPEGVHKEYKEDPKRCHDGTIEFTSIDAHNGVAPSR
RGDLEILGYCMIQWLTGHLWPEDNLKDPKYVRDSKIRYRENIASLMDKCFPEKNKPGEIA
KYMETVKLLDYTEKPLYENLRDILLQGLKAIGSKDDGKLDLSVVENGLAKTTKKRKK
EIEESKEPGVEDTEWSNTQTEEAIQTRSRTRKRVQK

N-glycosylation site.

57-60

cAMP- and cGMP-dependent protein kinase phosphorylation site.

147-150

Tyrosine kinase phosphorylation site.

160-167

188-194

241-249

295-302

N-myristoylation site.

40-45

46-51

235-240

347-352

369-374

Cell attachment sequence.

241-243

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

37-325

FIGURE 33

AGTTGGCGGGAATGGCTGCTCGGGAGGGCAGTGTACCGGGGGCCGCTGTAGGCTGTCC
 AGCGATGGATCCCACCGCGGGAAAGCAAGAAGGAGCCTGGAGGGAGGCGCGACTGAGGA
 GGGCGTGAATAGGATCGCAGTGC~~CAA~~AGCCGCCCTCATTGAGGAATTCAAGCATAGTGAA
 GCCCATTAGCCGGGGCGCCCTCGGGAAAGTGTATCTGGGGAGAAAGCGGCAAATGTAA
 TGCA~~GT~~AAAGGTTGTTAAAAAAGCAGACATGATCAACAAAATATGACTCATCAGGTCCA
 AGCTGAGAGAGATGCACTGGCACTAAGC~~AA~~AGCCATTCA~~TT~~GTCCATTGTATTTC
 ACTGCAGTCTGCAAACAAATGTCTACTTGGTAATGGAATATCTATTGGGGAGATGTCAA
 GTCTCTCCTACATATATATGGTTATTTGATGAAGAGATGGCTGTGAAATATATTTCTGA
 AGTAGCACTGGCTCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACC
 GGACAATATGCTTATTTCTAATGAGGGTCATATTAAACTGACGGATTTGGCCTTCAAA
 AGTTACTTGAATAGAGATATTAATATGATGGATATCCTTACACACCATCAATGGCAA
 ACCTAGACAAGATTATCAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTGGG
 ATTTAACACACCAATTGCAAGAAAAAAATCAAGACCCCTGCAAACATCCTTCAGCCTGTCT
 GTCTGAACATCACAGCTTCTCAAGGACTCGTATGCCCTATGCTGTAGATCAAAGGA
 CACTACGCCCTATTCTAGCAAATTACTAAATCATGCTTGTGAAACAGTTGCCCTCAACCC
 AGGAATGCCGTGAAGTGTCTAATTCTAATTACTCCAGTCTAGGAAAGGCTGGCAC
 ATCCAGTGCAGTAGTCATC~~CC~~ACACCTTCATATCCAGTGTGGAATCAGAATGCCACAG
 CAGTCCCAAATGGAAAAAGATTGCCAGGAAAGTGTATGAAAGCATTGGGCCAACAAATGAT
 GAGTTGAATGCA~~GT~~TTGAAAGTTATGCGCAAATCTGCAAATGCCATTGAGACGAAAGG
 TTTCAATAAAAGGATCTGGAGTTAGCTTTCTCCATTCAACAGCAGTGCCCTTCC
 CACCACTGGACGCTTGTGTAACCTGCTAAAAATGCTCTGGGAAGTTCTG
 GGAAGCAGTAGAAACTGGATGTAATAATATAATGGACACTGACACAAGTCAGTAGG
 TTTCCATCAGTC~~AA~~ATCAGTGGCTGTGGATTCTGGTGGGATATCTGAAGAGCACCCTGG
 GAAAAGAAGTTAAAAAGAATT~~TT~~GAGTTGGTGA~~CT~~CCAGTCTGTGAAAGGTTAT
 ACAGAATAAAACACTGTGTAGAGTATAAGCATAACGAAATGACAAATTGTTATACAAA
 TCAAAATACAGGCTTAACAGTGAAGTGCAGGACCTTAAGCTATCAGTGCACAAAGTC
 AC~~AA~~ATGACTGTGCTAATAAGGAGAACATTGCAATTCTTTACTGATAAACAAAC
 ACCAGAAAAATTACCTATACCAATGATAGC~~AA~~ACCTTATG~~GT~~GAACTCGATGAAGA
 CTGTGAAAGAATAGTAAGAGGGACTACTTAAGTTCTAGTTTCTATGTTCTGATGATGA
 TAGAGCTTCTAAAAATTCTATGAACTCTGATTCATCTTCTGGAAATTCTATAAT
 GGAAAGTCCATTAGAAAGTCAGGCCCTAGATT~~C~~AGATAGAAGCATTAAAGAATCCTTT
 TGAAGAATCAAATATTGAAGATCCACTTATTGTAACACCAGATGCCAAGAAAAGACCTC
 ACCAAAAGGTGCGAGAACCTGCTGTACAAGAGAGTAACCAAAATGTTAGGTCCCTCC
 TTTGGAGGTGCTGAAACGTTAGCCTCTAAAAGAAATGCTGTTCTGGAAAGTTAA
 CAGTCATATTAAATGCA~~TC~~AAACTCAGAACCATCCAGAATGAAACATGACTTCTTTAGA
 TGCAATGGATATTGGCTGCTACAGTGGTTCATATCCCATGGCTATAACCCCTACTCA
 AAAAAGAAGATCCTGTATGCCACATCAGACCCCAAATCAGATCAAGTGGAACTCCATA
 CCGAACTCCGAAGAGTGTGAGAAGAGGGGTGGCCCCGTTGATGATGGCGAATTCTAGG
 AACCC~~CC~~AGACTACCTG~~C~~ACCTGAGCTTACTAGGCAGGCCATGGCTGTGGTAGA
 CTGGTGGGCACTTGGAGTTGCTTGTGAAATTCTAACAGGAATTCCCCCTTCAATGA
 TGAAACACCACAAAGTATT~~C~~AGAATATTCTGAAAGAGATATCCCTGGCCAGAAGG
 TGAAGAAAAGTTATCTGATAATGCTCAAAGTGCAGTAGAAATACTTTAACCAATTGATGA
 TACAAAGAGAGCTGGAATGAAAGAGCTAAACGTCATCCCTCTTCTCAGTGTGACTG
 GGAAAATCTGCA~~G~~CATCAGACTATG~~C~~TTCTCATCCCCCAGCCAGTGTGAAACAGATAC
 CTCCTATTGAAACAGGAATACTGCTCAGCACCTGACCGTATCTGGATTAGTCTGTA
 GCACAAAAATTCTTCTTCTAGTCTAGCCTCGTGTATAGAATGAAACTTGCAATAATTAT
 ACTCCTTAATAACTAGATTGATCTAAGGGGAAAGATCATTATTAAACCTAGTTCAATGTG
 CTTTAATG~~T~~ACGTTACAGCTTACAGAGTTAAAGGCTGAAAGGAATATAGTCAGTAA
 TTTATCTTAACCTCAAAACTGTATATAATCTTCAAAGCTTTTCATCTATTATTG
 TTTATTGCACTTATGAAAGACTGAAGCATCAATAAAATTAGAGGACACTATTGAGAGTGA
 GCCACTAGCTGATTCTTCTTCTGATTTCAGTTCACTGTTCA~~G~~TTCAGTTAGCATTAAA
 ATAATAAAATAATCATA~~C~~AGT~~CC~~

FIGURE 34

MDPTAGSKKEPGGAAATEEGVNRIAVPKPPSIEEFISIVKPIISRGAFGKVYLQKGGKLYA
 VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
 LLHIYGYFDEEMAVKYISEVALALDYLHRGIIHRDLKPDNMLISNEGHIKLTDGFLSKV
 TLNRDINMMDILTPPSMAKPRQDYSRTPGQVLSLISLGFNTPIAEKNQDPANILSACLS
 ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
 SASSQSHTFISSVESECHSSPKWEKDCQESDEALGPTTMSWNAVEKLCAKSANAIETKGF
 NKKDLELALSPHIHNSSALPTTGRSCVNLAKKCFSGEVSWEAVELDVNNINMDTDTSQLGF
 HQSNQWAVDGGISEEHLGKRSLSKRNFEVDSSPCKIIQNKKTCEYKHNEMTNCYTNQ
 NTGLTVEVQDLKLSVHKSQQNDANCENIVNSFTDKQQTPEKLPPIPMAKNLMCCELDED
 EKNSKRDYLSSSFLCSDDDRASKNISMNSDSSFPGISIMESPLESQPLDSDRSIKESSFE
 ESNIEDPLIVTPDCOKEKTPKGVENPAVQESNQKMLGPPLLEVLTASKRNAVAFRSFNS
 HINASNNSEPSRMNMTSLDAMDISRAYSGSYPMAITPTQKRRSCMPHQTNPQIKSGTPYR
 TPKSVRGVAPVDDGRILGTPDYLAPELLGRAHGPADVWALGVCLFEFLTGIPPFNDE
 TPQQVFQNLKRDI PWPEGEEEKLSDNAQSAVEILLTIDDTKRAMKELKRHPLFSDVDWE
 NLQHQTMPFIPQPDDETDSYFETRNTAQHLTVSGFSL

N-glycosylation site.

73-76
 374-377
 564-567
 663-666
 666-669
 674 -677

cAMP- and cGMP-dependent protein kinase phosphorylation site.

700-703

N-myristoylation site.

12-17
 13-18
 52-57
 209-214

Amidation site.

438-441

Serine/Threonine protein kinases active-site signature.

152-164

Protein kinase domain

35-834

FIGURE 35

CAAGAGCCCTTCCTGCAGGGAACCTCAGGCTTCAGAGAGCCAAAAAGTTGGGAGGCCTAA
CCACTTACAGGCCGGAAAGTGTCCGGGTGGACGCATTGGTAGCCGAAGAAGTCCOAGG
ATTGCCGAAGAAGTCCCAGGATTCCGAAGCGAGCCGAAGCATTGGGACAGTTTCAGAG
ACAGCTGATCGGTTGGAGCTGTGCGCCGAGCAGTCATGGCGGGCCAGAGCTACTACG
CCGGCCGATGGCGAGGGAGCCGCCCGGAGGCTGAGGCTCTGGCGAGCCGGAAACGG
AGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGGCGAGGCCGCGTGTTC
CGTGGCCGCTTCCAGGGCCGCGCGCGGTGATCAAGCACCGCTCCCCAAGGGCTACCGG
CACCCGGCGCTGGAGGCAGCGGCTTGGCAGACGGCGACGGTGCAAGGAGGCCGGCGCTC
CTCCGCTGTCGCCGCGCTGGAATATCTGCCCACTGGTGTCTTTTGTGGACTATGCTCC
AACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAATGTTGAGATTATATTCAAGTCC
ACTATGGAGACTGAAAAAAACTCCCCAGGGTCTCTCCAACTTAGCCAAGACAATTGGCAG
GTTTTGGCTCGAATGCACGATGAAGAACCTCATTGATGGTCACTCACCACCTCCAACATG
CTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTGGGCTGAGTTTC
ATTTCAAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTC
AGTACCCATCCAAACACTGAAACTGTGTTGAAGCCTTCTGAAGAGACTACTCCACCTCC
TCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCCTGAGAGGAAGAAAG
AGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACAGTGAAGCTTTTTC
AAAGTAAATTGAGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGAT
ATTAaaaaaaaaaaaaaaaaaaaaaaaaaaaa

FIGURE 36

MAAARATT PADGEE PAPEAEALAAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEIEGSV
TVRDYIQSTMETEKT PQGLSNLAKTIGQVILARMHDEDLIHGDLTTSNMLKKPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

cAMP- and cGMP-dependent protein kinase phosphorylation site.

78-81
247-250

N-myristoylation site.

147-152

Amidation site.

76-79
245-248

Tyrosine protein kinases specific active-site signature.

158-170

Protein kinase domain

33-252

FIGURE 37

AGCGCGCGACTTTGAAAGCCAGGAGGGTTCGAATTGCAACGGCAGCTGCCGGCGTAT
GTGTTGGTCTAGAGGCAGCTGCAGGGTCTCGCTGGGGCGCTCGGGACCAATTGAA
GAGGTACTTGGCCACGACTTATTTCACCTCCGACCTTCCAGGCGGTGAGACTCT
GGACTGAGAGTGGCTTCACAATGGAAGGGATCAGTAATTCAAGACACCAAGCAAATTA
TCAGAAAAAAAGAAATCTGTATTATGTTCAACTCCAACATAAAATATCCGGCCTCTCG
TTTATGCAGAAGCTGGCTTGGTACTGGGTAATGTGACCTAATGAAAAGATCTCCA
AGAGGTTTGTCTCATTCTCCTGGGCTGTAAAAAGATTAATCCTATATGTAATGATCAT
TATCGAAGTGTGATCAAAGAGACTAATGGATGAAGCTAAGATTGAAAAGCCTTCAT
CATCCAAACATTGTTGGTTATCGTGTCTTACTGAAGCCAATGATGGCAGTCTGTGTCTT
GCTATGGAATATGGAGGTGAAAAGTCTAAATGACTTAATAGAAGAACGATAAAAGCC
AGCCAAGATCCTTCCAGCAGCCATAATTAAAGTTGCTTGAATATGGCAAGAGGG
TTAAAGTATCTGCACCAAGAAAAGAAACTGCTTCATGGAGACATAAAGTCTCAAATGTT
GTAATTAAAGGCGATTGAAACAATTAAATCTGTGATGTAGGAGTCTCTACCAACTG
GATGAAAATATGACTGTGACTGACCCCTGAGGCTTGTACATTGGCACAGGCCATGGAAA
CCCAAAGAAGCTGGAGGAGAATGGTGTATTACTGACAAGGCAGACATAATTGCTT
GGCCTTACTTGTGGAAATGATGACTTTATCGATTCCACACATAATTCTCAAATGAT
GATGATGATGAAGATAAAACTTTGATGAAAGTGAATTGATGATGAAGCATACTATGCA
GCGTTGGGAACCTAGGCCACCTATAATATGGAAGAACTGGATGAATCATAACAGAAAGTA
ATTGAACTCTCTGTATGCACTAATGAAGACCCCTAAAGATGTCCTCTGCTGCACAC
ATTGTTGAAGCTCTGGAAACAGATGTCTAGTGTACATCTCAGCTGAAGTGTGGCTTGCGT
AAATAACTGTTATTCCAAAATTTACATAGTTACTATCAGTAGTTATTAGACTCTAA
ATTGGCATATTGAGGACCATAGTTCTGTTAACATATGGATAACTATTCTAATATGA
AATATGCTTATATTGGCTATAAGCACTTGGATTGTACTGGGTTCTGTAAAGTTTAG
AAACTAGCTACATAAGTACTTGTACTGCTCATGCTGACTTAAACACTAGCAGTAAA
CGCTGTAAACTGTAACATTAAATTGAATGACCATTACTTTATTAAATGATCTTCTTAA
TATTCTATATTAAATGGATCTACTGACATTGACTTGTACAGTACAAAATAAGCT
ACATTGTTAAAACACTGAACCTTGTGATGTGTTATCAAATGATAACTGGAGCT
GAGGAGAATATGCCTCAAAAAGAGTAGCTCTGGATACTTCAGACTCTGGTTACAGATT
GTCTTGATCTGGATCTCCTCAGATCTTGGTTTGCTTTAATTAAATGTATT
TTCCATACTGAGTTAAAATTAAATTGTACCTTAAGCATTCCAGCTGTGTAAA
ACAATAAAACTCAAATAGGATGATAAGAATAAAGGACACTTGGTACCAAGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MEGISNFKTPSKLSEKKKS VLCSTPTINIPASPFM QKLGFGTGVNVYLMKRS PRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGG
KSLNDLIEERYKASQDPFPAAIILKVALN MARGLKYLHQEKLLLHGDIKSSNVVIKGDFE
TIKICDVGVS LPLDENMTVTDPEACYIGTEPWKPKEA VEEENGVI TDKADIFAFGLTLWEM
MTLSIPHINLSN DDDDEDKTFDE SDFDDE AYYAALGTRPPINMEE LDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

N-glycosylation site.

196-199
249-252

cAMP- and cGMP-dependent protein kinase phosphorylation site.

16-19

N-myristoylation site.

41-46
118-123

Serine/Threonine protein kinases active-site signature.

163-175

Protein kinase domain
32-320

FIGURE 39

GTGCGATCCGGGCCCCGAGGGCATTAGACGGCGGCTGATTAGCTCCGGTTGCATCACCC
GGACCGGGGGATTAGCTCCGGTTGCATCACCCGGACC GGCGGGCCGGCGCGCACGAGAC
TCGGCAGCGGAAGTGGAGGCGCTCCGCGCGTCCGCTGCTAGGACCCGGCAGGGCTGG
AGCTGGGCTGGGATCCCAGCTGGCAGCAGCGCAGCGGGCCGGCCACCTGCTGGTGC
CTGGAGGCCTCTGAGCCCCGGCGCCGGCCACCGGAAACGACGGGGCGAGATGCCA
GCCACCCCTCTAGCTGCTCCTGCGGGTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT
GACAACCTAGATAACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA
CTGCCCCCTGCCTGTTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCACACTGCTGTG
GCCACTGCCTCCCGTCTGGGCCCTATGTCCTCCTGGAGGCCGAGGGCGGGCGGCC
TACCAAGGCCCTGCACTGCCCTACAGGCACTGAGTATACTGCAAGGTGACCCCGTCCAG
GAAGCCCCGGCGTGTGGAGGCCCTATGCCGGCTGCCCGACAAGCATGTGGCTCGG
CCCACTGAGGTCTGCTGGTACCCAGCTCCTTACCGCTTTCACTCGGACCCATGGG
GACATGCACAGCCTGGTGCAGGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC
TTCCGCCAGATGGCCACCGCCCTGGCGACTGTCAACAGCACGGTCTGGTCTGCCGTGAT
CTCAAGCTGTGCTGCTTGTCTCGTGTACGGCCAGATGATCCCTGTTGGACAAGCACCGTGC
CTGGAGGACTCCTGCGTGTACTGGCCAGATGATCCCTGTTGGACAAGCACCGTGC
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGCCTCATACTCGGGCAAGGCAGCC
GATGTCGGAGCCTGGCGTGGCGTCTCACCATGTCGGCCGCCACTACCCCTCCAG
GACTCGGAGCCTGTCTGCTCTCGCAAGATCCGCCGGGGCTACGCCCTGCCGTGCA
GCCCTCTCGGCCCCCTGCCCGTGTCTGGTCTGCCCTCGTGGGAGCCAGCTGAA
CGGCTCACAGCCACAGGCATCCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA
GCCCAACCCGATCCCATCTCTGGAGGCTGCCAGGTGGTCCCTGATGGTCTGGGCTG
GACGAAGCAGGGAAAGGAGGAGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCC
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTGGGGTAGCTCCAAGCCTCTCCTG
CCTCTGAACATGAGCCAAACCTTCAGTCAGCTTCCAGAAGGGAGAAAGGCAGAACGCTGT
GGAGTGTGCTGTGACACATGCTTGTCCACACATGCAAGTCCCTGCTGGGTGCT
TATCAGGTGCCAAGCCTGTTCTGGTGTGGAGTACAGCAGTGAGCAAGGAGACAAT
ATTCCCTGCTCACAGAGATGACAAACTGGCATCCTGAGCTGACAACACTTTCCATGAC
CATAGGTCACTGTCTACACTGGGTACACTTGTACCAAGTGTGCCCTCACTGATGCTGG
TGCTCAGGCACCTCTGCTCAAGACAATCCCTTCACAAACAAACCAGCTGCCCTTGAT
CTTGTACCTTTCAAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCC
GCAACTCAGGACCCAAGCCCAGCTCACTGTTCCAGCAGTCTGTCC
TGATTAAGAGATTCTCCTCCAGGCATAAGCCTGGGATTGGCCAGAGATAAGAATCC
AAACTATGAGGCTAGTTCTGTCAACTCAAGACTGTTCTGGAAATGAGGGTCCAGGCCTG
TCAACCATGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGCTG
TCCCTGTGGGCCACCTGAAAGTCCCAGGTGGACTCTCTGGGGACACTTGGGGTCCACAA
TCCCAGGTCCTACTCTAGGTTGGATACCATGAGTATGTATGTTACCTGTGCCCTAAT
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAA

FIGURE 40

MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGPQPRILPPCLLPLSPPTAPDRAT
AVATASRLGPYVLLPEEGGRAYQALHCPTGTEYTCVYPVQEAPAVLEPYARLPPHKHV
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRRIPEPEAAVLFRQMATALAHCHQHGLVL
RDLKLCRFVFADEKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
AERLTATGILLHPWLQRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG

N-myristoylation site.

91-96
341-346

Protein kinase domain

71-315

FIGURE 41

GAAGTTCTCACTAGGGTCTTCTGGCCCAGCCTTGACTGAAGCTGGCTGGAGACAG
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCAGGGCCACTCAAGGACCCAGG
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCCATTGCCCTTGAGAGAA
AGAAGAGGACCCGGTGAAACATGCTGCTGTAAGAAAACACAGGAGGACATCAGCAGCG
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTCTCCGAGGTGGTCTGGCCAGG
AGCAGGGCTCCGACACCTCGTGGCCCTCAAGTGCATCCCAAGAAGGCCCTCCGGGGCA
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCAAACATCG
TCGCTCTGGAGGATGTCCACGAGAGGCCCTCCACCTTACCTGCCATGGAACCTGGTGA
CGGGTGGCGAGCTGGTACCGCATCATGGAGCGCGCTCCTACACAGAGAAGGATGCCA
GCCATCTGGTGGGTCAAGGCCTGGCGCGTCTCCTACCTGCACAGCCTGGGATCGTGC
ACCGGGACCTCAAGCCGAAACCTCCTGATGCCACGCCCTTGAGGACTCGAAGATCA
TGGTCTCTGACTTTGGACTCTAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG
GGACCCCTGGATATGTGGCCCCAGAGCTTGGAGCAGAAACCCCTACGGGAAGGCCGTAG
ATGTGTGGCCCTGGCGTCATCTCCTACATCCTGCTGTGGTACCCCCCTTCTACG
ACGAGAGCGACCCCTGAGCTTCAAGCAGATCCTGAGGCCAGCTATGAGTTGACTXTC
CTTCTGGATGACATCTCAGAATCAGGCAAAGACTTATTGGCACCTCTGGAGCGAG
ACCTTCAGAAGAGGTTCACCTGCCAACAGGCCCTGGGGACCTTGGATCTTGGACA
CAGGCTTGGCAGGGACATCTAGGGTTGTCAGTGAGCAGATCCGGAAAGAACTTGTCTT
GGACACACTGGAAGCGAGCCTCAATGCCACCTTGTCTGCCACATCCGGAAAGCTGG
GGCAGATCCCAGAGGGCGAGGGGCCCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG
GCCTTCGTGCTGGCCAGCCCCCAAGTGGTGATGCCCAGGXAGATGCCGAGGCCAAGTGG
AXTGAXCCCCAGATTXCTTXC

46/46

FIGURE 42

MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGSAHLVALKCIPKKALRGKEALVEN
EIAVLRRISHPNIVALEDVHESPSHLYLAMELVGGELFDRIMERGSYTEKDASHLVGQV
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTPGYVA
PELLEQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDXPFWDDIS
ESGKDFIRHLLERDLQKRFTCQQLRDLWIWDTGFGRDILGFVSEQIRKNFAWTHWKRA
FNATLFLRHIRKLGQIPEGEQGASEQGMXRSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8
66-69
257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123
166-171
170-175
334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

15-270